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US-10-510-941-2 Perfect score:

1542 1 LETLLELKOVSKTIRGKKII......KSLEDRFLEITADKEEAQHV 307 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Geneseq\_8:\* geneseqp1980s:\* geneseqp1990s:\*

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp20048:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

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S		Description	Adn97355 B. lichen	Ads27585 Bacterial		Abu32480 Protein e	Abb48180 Listeria	Adg32114 Mutant B	Abu44428 Protein e	Ads28089 Bacterial	Adn27185 Bacterial	Adn48041 Thermococ	Ads41933 Bacterial	Adn18644 Bacterial	Adn18683 Bacterial	Adn46530 Thermococ	Ads27537 Bacterial	Aee95518 E. faecal	Adn46418 Thermococ	Aab96628 Putative	Ads43172 Bacterial	Abu25506 Protein e	Adc97283 E. faeciu	Aab96710 Putative	Abp26280 Streptoco
SUMMARIES		ΩI	ADN97355	ADS27585	ABB47477	ABU32480	ABB48180	ADG32114	ABU44428	ADS28089	ADN27185	ADN48041	ADS41933	ADN18644	ADN18683	ADN46530	ADS27537	AEE95518	ADN46418	AAB96628	ADS43172	ABU25506	ADC97283	AAB96710	ABP26280
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ABU26098	ADB11670	ADN46668	ABP26335	ADV88530	ADV81939	ADV79783	ADS22213	ABB09645	ABG72543	ADU80820	ADS29173	ADN47270	ABU24420	ADS29082	ADS29721	ADS22132	ADC94125	AAG92767	ADN46278	ADS27622	ADN18549
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285	377	328	300	300	300	300	311	233	233	233	297	302	310	305	316	233	332	312	306	308	312
29.0	29.0	28.8	28.7	28.7	28.7	28.7	28.4	28.3	28.3	28.3	28.2	28.2	28.0	28.0	28.0	27.9	27.9	27.8	27.8	27.6	27.5
447.5	447.5	444	442	442	442	442	438	436	436	436	435.5	434.5	432.5	431.5	431.5	430.5	430.5	429	428.5	425	424.5
24	25	56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

antibiotic synthesis; proteolytic; protease. Š ADN97355 standard; protein; 307 (first entry) 01-JUL-2004 ADN97355; RESULT 1 ADN9735 GCCCCCCCCX8X4444X88X1X8X8X8X8X8X8X8X8X8X8X

B. licheniformis antibiotic synthesis related protein SEQ ID NO:2.

Bacillus licheniformis.

WO2003087142-A2. 23-OCT-2003. 25-MAR-2003; 2003WO-DK000199. 10-APR-2002; 2002DK-00000532.

(NOVO ) NOVOZYMES AS.

Rasmussen MD, Olsen PB, Clausen IG; Andersen JT, Jorgensen ST, WPI; 2003-833704/77. N-PSDB; ADN97354. New Bacillus licheniformis mutant host cell that is mutated in one or more gene(s) encoding one or more polypeptide(s) having proteclytic activity, useful for producing, isolating and/or purifying at least one product of interest.

Disclosure; SEQ ID NO 2; 100pp; English.

The invention relates to a novel Bacillus licheniformis mutant host cell derived from a parent B. licheniformis host cell, where the mutant host cell is mutated in one or more gene(s) encoding one or more polypeptide(s) having proteolytic activity that is at least 80% identical to any of the 22 amino acid sequences fully defined in the specification, where the mutant host cell expresses at least 5% less of one or more polypeptide(s) having a proteolyric activity than the parent host cell, when they are cultivated under comparate conditions. The host cell is useful for producing at least one product of interest, and for isolating or purifying the product of interest. The present sequence represents an

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useful for producing plants with improved properties
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.5<sup>3</sup>
Matches 147; Conservative
  source,
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 microbial
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                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                  GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
                                                                                                                                                             EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR
                                                                                                                                                                                                EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITAD
                                                                            LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                             LETLLELKNVSKTIRGKKI1EGLSFDVRAGE1FGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                             IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
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                                       Length 307;
  antibiotic synthesis related polypeptide of the invention
                                                        Indels
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                                      Query Match 100.0%; Score 1542; DB 7; Best Local Similarity 100.0%; Pred. No. 3e-130; Matches 307; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                   Bacterial polypeptide #16618,
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SLATER S C.
CHEN X.
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                      Sequence 307 AA;
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(CHEN/)
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promote functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant such as maize or soybean. The method of producing a transformed plant countries or soybean. The method of producing a plant with the secondinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improved plant with the recombinant DNA construct is useful for improved plant with the polynucleotide or polypeptide is useful for improved plant properties. CT the recombinant DNA construct is useful for improved plant properties, ct improved plant properties, extreme osmotic conditions, pathogens or peats, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth race by modification or prosent, increased rate of content, improved yield by modification of farbohydrate, introgen or phosphorus use and/or uptake, by modification of farbohydrate, introgen or phosphorus use and/or uptake, by modification of farbohydrate, introgen or providing improved lighin production or improved galactomannan condition, improved lighin production or improved dia for the grampate of the printed specification but was obtained in electronic corner from part of the printed specification but was obtained in electronic corner from user of order or the printed specification or second to t
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48.5%; Pred. No. 7.8e-58;
ive 66; Mismatches 81;
Claim 1; SEQ ID NO 16618; 122pp; English.
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ABU32480 standard; protein; 301 AA

RESULT 4 ABU32480 ABU32480;

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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic colymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and constitution and biodegradation, especially biosynthesis of Vitemain B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes related diseases. In addition, the genome caquence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed general columns in the properties of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification and models and proteins encoded by the printed specification and models and proteins encoded by the printed specification, but was obtained in the printed proteins and proteins encoded by the printed specification and models and proteins encoded by the printed specification and models and proteins encoded by the printed specification and proteins encoded by the proteins encod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
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                                                                                                                                                                                                                                                                                                                            Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihl H, Dehoux P, Dussurget O, Chetouani F, Neddari H, dlaser P, Kunst F, Cossart P). Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Varquez-Boland JA, Domaniels G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charlat A, Durant L, Perez-Diaz J, Baquero F, Garcia D Portillo F, Gomez-Lopez N, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AVCGVSVKENFEKAARHIGALVENPELYKFLIGYQNLQQYARMTKGVTKKKIDELVELVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 182; 192pp; French.
                                                                                                                                                               11-APR-2001; 2001WO-FR001118.
                                                                                                                                                                                                                      11-APR-2000; 2000FR-00004629
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Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-010914/01.
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The invention relates to an isolated nucleic acid comprising any one of the invention relates to an isolated nucleic acid inhibits proliferation of a cell. Also included are:

Co f the nucleic acid inhibits proliferation of a cell. Also included are:

Co in a vector comprising a promoter operably linked to the nucleic acid model as promoter operably linked to the nucleic acid concluded are:

Co encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of agene in a operon required for proliferation or the activity of agene in an operon required for proliferation or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene product or that has an activity against a biological pathway in which a proliferation-required gene product or the proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for a collection and activity and activity of a compound acids required for collection of an organism. The antisense nucleic acids are useful for a conting for a solution and acids required for a solution and accenting for homologous nucleic acids required for a solution of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antiaense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                                                                     Protein encoded by Prokaryotic essential gene #18007
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                      Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zamudio C,
Trawick JD,
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                                                                       19-JUN-2003
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Wall D,
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monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and corbisosynthesis and blodegradation, especially blosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                       62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMT-KGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                           123 KLTGAINQKVKTYSLGMRQRLGVAQALIHSPALLILDEPTNGLDPQGMAEFRTLIRDLA- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GLKARINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                             2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant; host cell; production yield; shelf life; product stability;
                                                                                                                                                                                                                                                                                           41.4%; Score 639; DB 5; Length 306;
45.3%; Pred. No. 7.1e-49;
ive 57; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutant B_licheniformis secreted polypeptide SeqID 84.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.3
Matches 135; Conservative
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N-PSDB; ADG32113.
                                                                                                                                                                                                                                                                  Sequence 306 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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                                                                                                                                                                                                    63 LIGGKDIRKNFTEAMRGLGSIVENPEFYTFLTGQENLAYFARMDSSIKKERIQEVTELVG 122
                                                                                                                                                                                                                                                                                                                 KGMAVIVSSHLLSEMELMCDRIAIIQNGK-LRDIQHVHGPARDEKKRYYIQADDTQALTR 240
                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L.
                                                                                                                                                                                                                                                                                                                                                                               EAAAF-RKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchrieser C, Frangeul L, Couve B, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Checuani F, Nedjari H, Glaser P, Kunst F, Cossart P Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Chakrin A, Amend A; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez M, Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                         62 AVCGVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVELVG
                                                                                                                       2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; gene therapy; vaccine, biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                       8;
                                                       Length 301;
                                                                                     81; Indels
                                                         DB 6;
                                                         ; Score 734; DB 6;
; Pred. No. 1.9e-57
61; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO 885; 192pp; French.
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                                                         47.6%;
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                                                                    Local Similarity 49.8%
nes 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes
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                          Sequence 301 AA;
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                                                                         Best Local Sim
Matches 149;
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                                                          Query Match
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Clausen IG;

Olsen PB,

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This invention relates to a novel Bacillus licheniformis (B. licheniformis) mutant host cell derived from a parent B. licheniformis host cell that is mutated in genes encoding secreted polypeptides.

Specifically, it refers to the generation of an improved Bacillus host that reduces the need for product purification caused by contaminant secreted native polypeptides in the culture medium. Accordingly, the present invention describes reducing the expression of these native proteins (e.g. proteolytic enzymes nutrient uptake factors and signal molecules), which in turn makes it easier to purify the heterologous product of interest and therefore improving the production process. Further benefits of a mutated host cell include an increase in total production yield and a longevity of shelf life attributable to improved product stability and purity. This polypeptide is a mutant B.
                   New mutant Bacillus licheniformis host cell secreting 5 % less of more secreted polypeptides than the parent host cell, useful for producing a product of interest e.g. polypeptides, amino acids or
                                                                                                                                                Claim 1; SEQ ID NO 84; 422pp; English.
                                                                                                    carbohydrates.
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Sequence 309 AA;

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GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLKN 124
                                                                                                                                                                                                     RINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGM 184
                                                                                                                                                                                                                         185 AVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARD-EKKRYYI----QADDTQALT 239
                                                                                                                                                                                                                                                                                       240 REAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEI 297
                                                                                                                                                                                                                                                                                                                                                         LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC
                                    10; Gaps
Query Match 41.4%; Score 638; DB 8; Length 309; Best Local Similarity 44.0%; Pred. No. 8.8e-49; Matches 131; Conservative 66; Mismatches 91; Indels 1
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                               Protein encoded by Prokaryotic essential gene #29955.
ABU44428 standard; protein; 302 AA
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                             21-MAR-2002; 2002WO-US009107.
                                          19-JUN-2003 (first entry)
                                                                                                             Streptococcus mutans,
                                                                                                                                 WO200277183-A2.
                                                                                                                                                       03-OCT-2002
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the invention trained by the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense contest and is a nucleic acid, (2) a host cell containing the vector; (3) an isolated continued to polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway confirmed for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity; (11) a culture compound that inhibits the extent or organism or the strains is present in a culture or collection of conduct is overexpressed or underexpressed; (12) determining the extent or product is overexpressed or underexpressed; (12) determining are useful for proliferation of an organism. The antise molecular for rational collection of configuration of an organism. The antise molecular sequired for cellular proliferation to solution or the configuration of an organism. The antise molecular acids are useful for for cellular proliferation to solution or the configuration of an organism or screening for homologous nucleic acids are useful for the description of the compound that inhibits the configuration of the configuration of the compound organism.
                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                          Ohlsen KL,
Forsyth RA,
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                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 72352; 1766pp; English.
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                                                                                                                                          Malone C,
Carr GJ,
08-FEB-2002; 2002US-00072851.
                                                                                  (ELIT-) ELITRA PHARM INC.
                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                             WPI; 2003-029926/02
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                                                                                                                                             Wang Wall
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3, 123 64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123 184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243 63 64 65 FDKNFDSNQIALLSSVGSLIEEPSYYANLTGYENLEIIQRILK-LPKENIDKVLKIVKLY 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV 124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG Gaps 4. 34.8%; Score 536; DB 6; Length 302; 39.3%; Pred. No. 1.3e-39; ive 64; Mismatches 111; Indels Query Match
Best Local Similarity 39.3'
Matches 116; Conservative 184 셤 a 셤 ð ઠે 8 8 셤

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Length 306;

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ADS28089;

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Bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct; transformed plant; improved plant property,
241 MRKGFELEENQSIVLKDYNKTNIAAAVKVLVANDIDIYQVRMVRKSLEEVFLDMT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a recombinant DNA construct comprising a
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                                                                                                                                                                                     ADS28089 standard; protein; 306 AA
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                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial polypeptide #17122
                                                                                                                                                                                                                                                                                                                                  (first entry)
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SLATER S C.
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(CHEN/)

Cao Y,

CAOY/) (SLAT/)

HINK/

18-DEC-2003

Bacteria

Sequence 306 AA;

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                                                                                                                                                 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123
                                                                                                                                                                                                                126 KVADRKVQEYSLGMKQRLAIAAARLLANPRLVILDEPINGLDPAGIIEIRNLILKLPKEYG 185
                                                                                                                                                                                                                                                                  184 MAVIVSSHILISEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynuclectide encoding a polypeptide from a
                                                                                              99
                                                                                                                                                                                                                                                                                                                                 244 AF----RKVKVDEAEGGIELSIQKD-EVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                      242 TILQERGINVDTQARGLVWANDRSDEEIAQLVKAFVEKDIDVYRISDETSSLEEIFLQLT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLLLDEPTNGLDPAGIREIRDYLRKLTREKG
                                                                                LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                             6
                             Indels
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                             69; Mismatches 106;
Score 535.5; DB (
Pred. No. 1.5e-39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 9838; 122pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADN27185 standard; protein; 299
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34.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial polypeptide #9838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2004 (first entry)
 Query Match
Best Local Similarity 38.54
Matches 115; Conservative
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HINKLE G J.
SLATER S C.
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comparising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant a uch as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polymetotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for improving plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan compact of the invention. Note: The sequence data for this patent did not form part of the printed sepecification but was obtained in electronic form part of the printed sepecification but was obtained in electronic commant from USPTO at sequence.
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Sequence 299 AA;

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IGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLKNRINDKVKTYSLGMR 138
                                                                                                                                                            80 VGSLIESPSYYGHLSGYENLRIIATL-KGTPEKDIGRVLEIVRLENQKNKKTNQYSLGMK 138
                                                                                                                                                                                                                                  QRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVIVSSHLLSEMEL 198
                                                                                                                                                                                                                                                                                      MCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAAAFRKVKVDEAEGGIE 258
                                                                                          20 VSDLDLSVAEGAVYGFLGPNGAGKSTTLKMILGLVKPTAGSITVFGKTWNHRSRMSILKD 79
                                                                     20 IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVKENFEKA-ARH 78
                                    22;
                                                                                                                                                                                                                                                                                                                                                          259 LSIQKD------EVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                33.5%; Score 516; DB 8; Length 299; ilarity 41.0%; Pred. No. 8.3e-38; Conservative 53; Mismatches 96; Indels
                  Local Similarity
                                 Matches 119;
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   Query Match
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gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; addicine; forensic science; food; drug inspection; molecular biology; immunology.
                                                                             Thermococcus kodakaraensis KOD1 protein sequence SeqID1919
ADN48041 standard; protein; 311 AA.
                                                                                                                                                                           Thermococcus kodakaraensis.
                                                    01-JUL-2004 (first entry)
                                                                                                                                                                                                   WO2004022736-A1
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30-AUG-2002; 2002JP-00319011 29-AUG-2003; 2003WO-IB003597

This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least a tablerary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly the genome of a hyperthermostable archaebacterium, particularly the genome of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein concoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at 233 99 genome of organism particularly chips for analysis, applicable in 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV CGVSVKENPEKAARHIGAIVENPELYKFLTGYQNLQQYA---RMTKGVTKKKIDBIVELV GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQAD---------DIQALTREAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKS 24; Gaps DB 8; Length 311; 32.5%; Score 501; DB 8; Length 311 38.3%; Pred. No. 2e-36; tive 63; Mismatches 103; Indels Claim 9; SEQ ID NO 1919; 598pp; Japanese. ftp.wipo.int/pub/published\_pct\_sequences Method for disrupting targeted gene in thermostable bacterium and with genome studying gene structure and functions (NISC-) JAPAN SCI & TECHNOLOGY CORP. ADS41933 standard; protein; 306 AA. Matches 118; Conservative LEDRFLEI 297 T, Atomi H; WPI; 2004-257583/24. Similarity Sequence 311 AA; 02-DEC-2004 ADS41933; 121 234 290 Query Match Best Local 297 Imanaka ADS41933 ઠે g a ઠે 셤 유 셤 a SKAKKB ઠે ò ઠે 8

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241 VEPIDVGSLDLDAADLRL----EGQNRLVVYSERDIRVELLRMLESAGYTVLDVHLQEPT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial polypeptide #20363.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to proude for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such an amproved property comprises transforming a transformed plant comprised plant the method of producing a transformed plant the transformed plant with the crombinant DNA construct and growing the transformed plant, where the compliant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improved plant, where the improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions plants with increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or concern, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development condition, improved plant growth and development condition, improved plant growth and development condition or protection. This sequence represents a bacterial polypeptide used in the growth and plant growth but was obtained in electronic former forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
            Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; peet tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 20363; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slater SC,
                                                                                                                                                                                                                                                                                                                                                            20-FEB-2003; 2003US-00369493.
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GOLDMAN B S.
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SLATER S C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SLAT/)
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32.0%; Score 493; DB 8; Length 306; 36.4%; Pred. No. 1e-35; ive 67; Mismatches 91; Indels Similarity Sequence 306 AA; Best Local Simi Matches 118; Query Match

GVSVKENPEKAARHIGAIVENPELYKFLTGYQNLQQYA---RMTKGVTKKKIDEIVELVG 121 65 a 윱 ò

5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64

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48;

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. : ::|:: | | |:||:|: 226 LEGY-EIKIETKQPLPEL----EIPDIIRIEKTTENKAIIFAKSDIRESISEELAKKGI 279 The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with KGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE 241 LKWRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181 Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. 242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIK----------HLTDSGV Goldman BS; Chen X, Claim 1; SEQ ID NO 1297; 122pp; English. 279 RLYEVKAVNKSLEDRFLEITADKE 302 280 TIISLEIEEPSLEDVFLKTIYRRE 303 Š ADN18644 standard; protein; 308 Hinkle GJ, Slater SC, 20-FEB-2003; 2003US-00369493 21-FEB-2002; 2002US-0360039P Bacterial polypeptide #1297. (first entry) WPI; 2004-061375/06. GOLDMAN B S. HINKLE G J. SLATER S C. US2003233675-A1. CHEN X 02-DEC-2004 18-DEC-2003. 182 ADN18644; Bacteria. Cao Y, CAOY/) (HINK/) (SLAT/) GOLD/) CHEN RESULT 12 ADN18644 ద ઠ 유 ò 셤 셤 ò

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improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form at from USPTO at segdata.uspto.gov/sequence.html.
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Sequence 308 AA;

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121
                                                                                                                                     64 GYDIFKEPLKAKERLGFLPENATIYEELTAWRNLDFPASFYRMSKQEKEKRIEELLKLVG 123
                                                                                                                                                                                             241
                                                                                                                                                                               LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                  AAAFRKVKVDEAEGGIELSIQKDEVPDLIK----------HLTDSGV 278
                                                                                                                                                                                                                                                                                                                 228 LEGY-EIKIETKQPLPEL----EIPDIIRIEKTTENKAIIFAKSDIRESISEELAKKGI 281
                                                                          S LELKNVSKTIRGKKIIEGLSPDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC
                                                                                                                    GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYA---RMTKGVTKKKIDEIVELVG
                                                                                                                                                                                                                                        KGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE
                                Gaps
                              91, Indels 48;
32.0%; Score 493; DB 8; Length 308; 36.4%; Pred. No. 1e-35; tive 67; Mismatches 91; Indels
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               Similarity
               Best Local Simi
Matches 118;
 Query Match
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   ADN18683 standard; protein; 318
                       Bacterial polypeptide #1336.
                02-DEC-2004 (first entry)
          ADN18683;
ADN18683
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; nest tolerance; pathogen tolerance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.

US2003233675-A1 Bacteria

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P.

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The invention relates to a recombinant DNA construct comprising a provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprising the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of catbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. Improved plant growth and development under at least one stress condition. Improved lighin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form of form of the condition of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provi
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                            Goldman BS
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1336; 122pp; English.
                                                                                                                                            Chen X,
                                                                                                                                            Hinkle GJ, Slater SC,
               HINKLE G J.
SLATER S C.
                                                                                              GOLDMAN B S.
                                                                                                                                                                                          WPI; 2004-061375/06.
                                                                       CHEN X
                    (HINK/)
(SLAT/)
(CHEN/)
                                                                                            (GOLD/)
                                                                                                                                          Cao Y,
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31.9%; Score 491.5; DB 8; Length 35.2%; Pred. No. 1.5e-35; ive 78; Mismatches 97; Indels Best Local Similarity 35.2 Matches 112, Conservative Sequence 318 AA; Query Match

7;

31;

Length 318;

107 61 3 VIEVRNIRK-LYPKKIPLPFRKVEWFEALKGITFRVKKGELFGLLGPNGAGKTTTIKILT 52 GHMSITAGEIAVCGVSVKENFEKAARHIGAIVENPE-LYKFLTGYQNLQQYAR----MTKG 62 TLLEPSSGEAKVLGLDVVKDAREIRKRINLVARGERTLYWRLTAYENLRYFASIYYIPRR 4 LLELKNVSKTIRGKKI------IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIV

셤

ð 셤 Š 108 VTKKKIDEIVELVGLKNRINDKVKTYSLGMRQRIGLAQSLLHDPKLLILDEPTNGLDPAG 167 181 227 168 IREIRDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKR ઠે 음 8

용 8 용 8

281 YEVKAVNKSLEDRFLEIT 298 |: :||| |: :| 295 LSVEVKEPTLEDVFIKLT 312

RESULT 14

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant cauch as maize or soybean. The method of producing a transformed plant caving an improved property. The plant is a crop plant caving an improved property comprises transforming a plant with the caving an improved property comprises transforming a plant with the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                               184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
                                                                                                                                     242 PIPELRHEEITRVERLAPNRIILFARSDIREWLSQYLTSKGVTILSLEVEEPSLEDVFMK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                            --- AEGGIELSIQKDEVPDLIKHLIDSGVRLYEVKAVNKSLEDRFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldman BS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 16570; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                      ADS27537 standard; protein; 221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial polypeptide #16570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                              244 AFRKVKVDE----
                                                                                                                                                                                                                                                                              302 TIYGRDE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-061375/06.
                                                                                                                                                                                                                          297 ITADKEE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS27537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HINK/)
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                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism. selecting at least I arbitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly Thermococcus kodakaraensis KODI. The method is for targeting the disruption of a gene in the genome of an organism, which is applicable in cludying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 SVKENFEKAARHIGAIVENPELYKFLTGYONLOQYA---RMTKGVTKKKIDEIVELVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | | : | | : | | | DMSREPIKIKERIGYLPENATIYGELTAWKNLEFFANFYRMSNSEREKRITELLKRVGLW 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DARYRKAKTFSKGMKQRLLLAQALINDPELLILDEPTSGLDPEGAHLVKEVIRE-AKAEG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 LKNVSKIIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in
                                                                                                                                                                                                                        gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 IENLTKSYGTFRAVDGLTFDVKVGEVFGFLGPNGAGKTTTILSMLGIIIPDDGRIEILGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.8%; Score 490; DB 8; Length 309;
1larity 36.8%; Pred. No. 1.9e-35;
Conservative 70; Mismatches 108; Indels 16; Gaps
                                                                                                                                                                          Thermococcus kodakaraensis KOD1 protein sequence SeqID408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_seguences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 408; 598pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISC-) JAPAN SCI & TECHNOLOGY CORP.
        ADN46530 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-2003; 2003WO-IB003597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2002; 2002JP-00319011
                                                                                                                                                                                                                                                                                                                                                                      Thermococcus kodakaraensis.
                                                                                                                    (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atomi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-257583/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004022736-A1.
                                                                                                                    01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Simu
Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Imanaka T,
                                                              ADN46530;
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homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
```

Sequence 221 AA;

2; 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE 60 Gaps 5; Query Match
31.5%; Score 485; DB 8; Length 221;
Best Local Similarity 46.2%; Pred. No. 3.4e-35;
Matches 98; Conservative 51; Mismatches 61; Indels 180 REKGMAVIVSSHLLSEMBLMCDRIALIONGKL 211 a ઠે ઠે ద ઠે 셤 ò

completed: July 13, 2006, 13:43:55

Search co

AGE BLANK (USPTO)

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

July 13, 2006, 13:44:12 ; Search time 40 Seconds (without alignments) 738.464 Million cell updates/sec Run on:

US-10-510-941-2 1542 1 LETLLELKNVSKTIRGKKII.......KSLEDRFLEITADKEEAQHV 307 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ABC transporter (A	ABC transporter (A	Similar to ABC tra	ŭ	ABC transporter (A	_	transporter	ABC transporter (A		ABC transporter (A	ABC transporter, A	ABC transported MD	bacitracin transpo	bcrA protein - Bac	cdd4-like protein	probable ATP-bindi	probable ATP-bindi	ABC transporter (A	cdd4 protein - Clo	ABC-type MDR trans	hypothetical prote	ш	ABC transporter (A	ABC transporter, A	ABC-type MDR trans	ABC-type multidrug	daunorubicin resis	ABC-type multidrug	ABC transport prot
SUMMARIES	ΩI		AD1169	·	G96916	E69771	H96917		•						T31682	T09008	H71008			-								_	B3	T29454
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	Length	305	301	301	31;	308	316	306	306	300	306	247	306	300	306	295	308	318	307	301	314	30.	316	311	567	317	313	318	30,	312
de	Query Match	9.99	47.6	47.3	44.1	43.5	43.3	41.6	41.4	41.4	34.7	34.3	33.9	33.4	33.2	32.7	32.0	31.9	31.5	31.4	30.8	30.7	30.5	30.1	30.1	30.1	ď	29.3		28.8
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181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYXIQADDTQALTR 240

transposase (08) /	ABC transporter AT	ABC transporter AT	ABC transporter, A	ATP-binding protei	spar protein - Bac	ABC transporter (A	ABC transport prot	ABC transporter (A	gliding motility p	ABC transporter (A	hypothetical prote	ABC transporter (A	probable ABC-type	ABC transporter (A	probable ATP-bindi
F83781	F96932	AE2102	F87655	AE2008	140516	C69012	T43103	E96920	T44443	B83912	D72257	E84136	T36316	B83686	G71131
N	N	~	N	~	Н	~	~	7	~	0	~	N	N	~	~
106	258	339	311	331	456	312	298	310	298	310	327	282	317	301	312
7	8.0	28.0	27.9	27.8	27.6	27.5	27.5	27.4	27.3	27.3	27.3	27.3	27.3	27.2	27.2
28	~							_	_					_	
442.5 28.	431.5 2	431.5	430.5	428	425	424.5	424	422.5	421.5	421.5	421	420.5	420.5	420	420

## ALIGNMENTS

K (	RESULT 1
2 4	Dosac - Bacillus subrilis ABC transporter (ATP-binding protein) homolog vhcH - Bacillus subrilis
O	C;Species: Bacillus subtilis
00	C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004 C:Accession: D69822
· 64	R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
UA	C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch A.; Ehrlich, S.D.; Emmerson, P.T.; Entjan, K.D.; Errington, J.; Pabret, C.; Perrari, E
z	lature 390, 249-256, 1997
∢.,	Authors: Founger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallo, T. Leanner, D. Bonitz, A.; Gallo, M. Gallo, T. Leanner, D. Bonitz, A.; Gallo, M. Gallo, M
4 🔀	cent, o, marwood, o.k., manach, n, marmer, n, morsapher, s, mosuno, s, marro, min Coetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinoit
⋖	., Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauec
>	y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell Rieger, M.: Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
∢	A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serc
ro E-	keuchi, W.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama 
· «	Jatchors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
∢	Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
∢ ,	A, Reference number: A69580; MUID:98044033; PMID:9384377
∢ ^	AfAccession: D69822
< ≪	A;Aostacus presiminary; increar actu sequence not snown; transfaction not snown; A;Molecule type: DNA
Ø	A;Residues: 1-305 <kun></kun>
<b>∢</b> ′	A,Cross-references: UNIPROT:P54592; UNIPARC:UP10000660122; GB:Z99108; GB:AL009126; NID
∢ ∪	A;Experimental source: strain 168 C:Genetics:
A	A, Gene: yhcH
O I	C; Keywords: ATP; nucleotide binding; P-loop
E 12	F;20-209/Domain: ATP-binding cassette homology <abc> F;37-44/Region: nucleotide-binding motif A (P-loop)</abc>
	Query Match 66.6%; Score 1027; DB 2; Length 305;
	Best Local Similarity 65.1%; Fred. No. 1.36-57; Matches 200; Conservative 47; Mismatches 56; Indels 4; Gaps 2;
a	Qy 1 LETILELKNVSKTIRGKKIJEGLSFDVRAGEJFGFLGPNGAGKTTTJRMIVGHMSITAGE 60
Ď	DD 1 WKTVLELKNVTKNIRGRTIIDDLSFTIREGEVFGFLGFNGAGKTTTIRMWVGLMKLSKGD 60
•	
o	Qy 61 IAVCGVSVKENPEKAARHIGAIVENPELYKPLTGYQNLQQYARMTKGVTKKKIDEIVELV 120 ::    : : :    : : :
Ω	Db 61 VLICGQSITKEYAKAIKHIGAIVENPELYKFLSGYKNLQQFARMVKGVTKEKIDEVVELV 120

ij

121

62

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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <GLA>
A;Cross-references: UNIPROT:Q92DR3; UNIPARC:UPI0000CC33A; GB:AL592022; PIDN:CAC95982.1
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Age transporter, ATP-binding component CAC0138 [imported] - Clostridium acetobutylicum C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004 C; Accession: 036916 A; Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 MAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHV-HGPARDEKKRYYIQADDTQALTREA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 LIGGKDIRKNFTEAMRGLGSIVENPEFYTFLTGQENLAYFARMDPSIKKERIQEVTELVG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRINDKVKTY SLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVG
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                                                                                                                                                                                                                                                                                                           Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.1%; Score 680; DB 2; Length 31
46.0%; Pred. No. 9e-36;
tive 60; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                   89, Indels
                                                                                                                                                                                                                                                                                                        Query Match
47.3%; Score 730; DB 2;
Best Local Similarity 49.5%; Pred. No. 6.2e-39;
Matches 147; Conservative 57; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 46.0%
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: CAC0138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Listeria monocycogenes
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C; Jace: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C; Jaces: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
C; Jaces: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
R; Glaser, P: Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Accession: AD1169
A; Accession: AD1169
A; Accession: AD1169
A; Residues: 1-301 cGLA>
A; Residues: 1-301 cGLA>
A; Residues: 1-301 cGLA>
A; Cross-references: UNIPROT: QSYBY6; UNIPARC: UPI000054D48; GB:NC_003210; PIDN: CAC98834.1
A; Experimental source: strain EGD-e
C; Genetics:
A; Genetics:
A; Genetics:
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Similar to ABC transporter (ATP-binding protein) lin0750 [imported] - Listeria innocua (Species: Listeria innocua (Joace 27-Nov-2001 #text_change 31-Dec-2004 (Species: P. ) Dominguez-Bernal, G.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karet, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makathors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makathors: Comparative genomics of Listeria species.

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                            transporter (ATP-binding protein) lmo0756 [imported] - Listeria monocytogenes (stra:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AATVLNQYDLISKTNGVEIKLAKEEVPAVIELLVMQQIRIYEVKVITKSLEDRFLEMTGE 297
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                                                                                               EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEITAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.8*
Matches 149; Conservative
                                                                                                                                                                                                                         -KEEAQH 306
                                                                                                                                                                                                                                                                                       TKEEVQH 304
                                       181
                                                                                                  241
                                                                                                                                                                                                                            301
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GB: AE001437; PIDN: AAK78131.1
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ABC transporter (ATP-binding protein) homolog lin1677 [imported] - Listeria innocua (st
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Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 31-Dec-2004
Cipacession: Ab1642
Riclaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jonennguez-Bernal, G.; Manier, W.D.; Fsihi, H.D.; Jonens, Exeft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; P.A.; A.; A.; Comparative genomics of Listeria species.
A; Fittle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
43.3%; Score 667; DB 2; Length 318
Best Local Similarity 42.9%; Pred. No. 6.1e-35;
Matches 133; Conservative 69; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q97MP5; UNIPARC:UPI0000C9D8B;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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QNLEDRYIEL 307
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                                                                                                                                                          ABC transporter (ATP-binding protein) homolog ydbJ - Bacillus subtilis
C;Species: Bacillus subtilis
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Baron, S; Brusellu, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Harwood, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Labuber, J.; Lazarevoic, V.; Lee, S.M.; Levine, A.; Lou, T.M.; Parcio, S.; Maueell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schlach, S.; Shroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serok
A;Authors: Yoshikawa, H.F.; Zumetein, B.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, R; Tele: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044013; PRID:9384377
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A,Rebidues: 1-308 «KUN»
A;Cross-references: UNIPROT:P96605; UNIPARC:UP1000005FF63; GB:Z99106; GB:AL009126; NID:g
A;Experimental source: strain 168
                            244 SKLPFVYEVKNNBDKISAAIQYGTSPKVIABLMKNSVEVIEFYKEHKTLEDRFMQIVEGE 303
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42.7%; Pred. No. 3.1e-35;
iive 71; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: ATP; nucleotide binding; P-loop F;21-210/Domain: ATP-binding cassette homology <ABC>F;38-45/Region: nucleotide-binding motif A (P-loop)
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Matches 131; Conservative
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Query Match

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protein from GDSL (phospholipase B) family of lipolitic enzymes [imported] - Clostridium c; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004 C; Date: 1972201 Bsecon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, R; Nolling, J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. J. Bannett, G.M.; Roonin, B.V.; Smith, D.R. J. Bennett, G.M.; M.D.; Lee, M.J.; Pareference and Comparative Analysis of the Solvent-Producing Bacterium Classic A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-300 «KUR»
A;Cross-references: UNIPROT:Q97ETO; UNIPARC:UPI00000D7564; GB:AE001437; PIDN:AAK80967.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 CGVSVKENPEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 KSIKDKISTYSLGMKQRMGIAQALMKRPKLLILDEPTNGLDPAGINDLRNLIQRLSKEEK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.4%; Score 638; DB 2;
40.7%; Pred. No. 3.8e-33;
tive 85; Mismatches 97;
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Matches 122; Conservative
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Query Match
Best Local Similarity 38.55
Matches 115; Conservative
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45.3%; Pred. No. 3.4e-33;
tive 57; Mismatches 104; Indels
                             Indels
Best Local Similarity 45.0%; Pred. No. 2.5e-33;
Matches 134; Conservative 59; Mismatches 103;
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Best Local Similarity 45.3%
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ABC transporter (ATP-binding protein) BH0445 [imported] - Bacillus halodurans (strain C C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Species: D1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004 C; Accession: B83705 C; Accession: B83705 A; Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132 A; Accession: B83705 A; Acc
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Dacitracin transport protein bcrA - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 05-Oct-2004
C;Accession: 577627
R;Podlesek, Z.; Comino, A.; Herzog-Velikonja, B.; Zgur-Bertok, D.; Komel, R.; Grabnar, Mol. Microbiol. 16, 969-976, 1995
Mol. Microbiol. 16, 969-976, 1995
A;Title: Bacillus licheniformis bacitracin-resistance ABC transporter: relationship to A;Reference number: 877627, MUID:96059642; PMID:7476193
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-306 <POD>
A;Cross-references: UNIPROT:P42312; UNIPARC:UPI0000126845; EMBL:L20573; NID:g466477; PI
A;Experimental source: strain ATCC 9945A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                      61 VELFG--EKNPTRSIYKKIGSIIEYPGFYPNLTAEENLDIHRRWMKIENOKRINETLTWV 118
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                                                                                                                                                                                           1 HKYLVRTFNLTKKYKNTSVVENLNLNI BOGQI YGFLGKNGAGKTTTLRMI LGLMKI STGE
                                                                                                                                                                                                                                                                                                                                                                               235 VKEACSLIKNNINIKDYEIIGKDAIKVYEKINESSTIAKTLIKNDIELYEMSFSKDNLED
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                                                                                                                                                                1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                                                                                                                                                                            61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
                                                                                                                                                                                                                                                                                                                                                       GL-KNRI-NDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                179 TREKGMAVIVSSHLLSEMELMCDRIALIONGKLRDIOHVHGPARDEKKRYYIQADDTQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 TREAAAFRK----VKVDEAEG--GIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Keywords: antibiotic resistance; ATP binding; nucleotide binding; P-loop F;20-209/Domain: ATP-binding cassette homology <ABC>F;37-44/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
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                                                                          Length 306,
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                                                                     ; Score 523; DB 2; Length 30; Pred. No. 6.6e-26; 65; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98; Indels
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33.4%; Score 515; DB 2;
Best Local Similarity 36.6%; Pred. No. 2.1e-25;
Matches 113; Conservative 76; Mismatches 98;
                                                                        33.9%;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 RFLEIT 298
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                                                                                             Similarity
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                                                                                             Best Local Sim.
Matches 121;
    C;Genetics:
A;Gene: CAC2040
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R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97151
A;Status: preliminary
A;Molocule type: DNA
A;Residues: 1-306 <MUR>
A;Residues: 1-306 <MUR>
A;Coss-references: UNIPROT:Q97HH1; UNIPARC:UPI00000CA3C9; GB:AE001437; PIDN:AAK79999.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q97MBO; UNIPARC: UPI00000C9DFE; GB: AE001437; PIDN: AAK78269.1; A; Experimental source: Clostridium acetobutylicum ATCC824 C; Genetics:
                                                                                             185
                                                                                                                                           243
                                                                                                                                                              FGKDLKQHRLDILKNIGALVESPSYYPHLSGEDNLETVRKIVK-VPKSRIAEVLELVRLT 125
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                                           MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AF---RKVKVDEAEGGIELSIQKD-EVPDLIKHLIDSGVRLYEVKAVNKSLEDRFLEIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 528.5; DB 2;
; Pred. No. 2.3e-26;
49; Mismatches 57;
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Best Local Similarity 48.6%
Matches 101; Conservative
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A,Molecule type: DNA
A,Residues: 1-242 <KUR>
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R;Konz, D.; Klens, A.; Schorgendorfer, K.; Marahiel, M.A.
Cham. Biol. 4, 927-937, 1997
A;Title: The bacttracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecu A;Reference number: Z21058; MUID:98089193; PMID:9427658
A;Accession: T31682
A;Status: pre: 131682
A;Status: pre: DNA
A;Status: pre: DNA
A;Residues: 1-306 <KON>
A;Crosser-references: UNIPROT:Q955Y9; UNIPARC:UP100000AF215; EMBL:AF007865; NID:g4464275; A;Gene: bcrA
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A;Cross-references: UNIPROT:031054; UNIPARC:UP100000B5C5D; EMBL:AF026542; NID:g2502065;
A;Experimental source: strain FF22
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
C;Accession: T09008
R;Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
R;Hynes, W.L.; Ferretti, J.S.
R;
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                                    61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKK-IDEIVEL 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 VGLQHETKKIVGKFSLGMKQRLGIARALLHYPELSILDEPTNGLDPIGIKEMRRLIHSLA 179
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----TDSGVRLYEVKAVNK 288
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                                                                                                                                                                                                                                                                                                                                                                                          bcrA protein - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
C;Accession: T31682
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239 TREAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHL----
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                                                                                    Length 299;
                                                                                                                       Indels
                                                                                    32.7%; Score 504.5; DB 2;
39.4%; Pred. No. 9.4e-25;
iive 59; Mismatches 102;
C,Genetics:
A,Gene: scarces:
C,Keywords: R
P,20-209/Domain: ATP-binding cassette homology <ABC>
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289 ENLEDIF 295
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                                                                                                      Best Local Similarity
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

July 13, 2006, 13:40:51; Search time 298 Seconds (without alignments) 952.952 Million cell updates/sec Run on:

Title: Perfect score:

US-10-510-941-2 1542 1 LETLLELKNVSKTIRGKKII......KSLEDRFLEITADKEBAQHV 307 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 seqs, 925015592 residues Searched:

2849598

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_7.2:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			Q8eqi5 oceanobacil				bacillus	bacillus		bacillus												bacillus			Q637g1 bacillus ce		Q722f3 listeria mo	Q5kzf8 geobacillus	_	Q97mq4 clostridium	Q41ax1 exignobacte	
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SUMMARIES	ID	Q65M37 BACLD	YHCH BACSU	Q8EQIS OCEIH	Q61117_BACAN	Q6HLJ0 BACHK	Q4MSI3_BACCE	Q73BE3_BACC1	Q3EML1_BACTI	Q63E15_BACCZ	Q81G51_BACCR	Q6HAN5_BACHK	Q81JQ2_BACAN	Q3EW61_BACTI	Q72X49_BACC1	Q4MLR2_BACCE	Q814M7_BACCR	Q81AB3_BACCR	Q630K0_BACCZ	Q8Y8Y6_LISMO	Q6HFD4_BACHK	Q733F8_BACC1	Q4MNN2_BACCE	Q92DR3_LISIN	Q4EUC2_LISMO	Q637G1_BACCZ	Q4ELV1_LISMO	Q722F3 LISMF	Q5KZF8_GEOKA	Q81TB0_BACAN	Q97MQ4_CLOAB	Q41AX1_9BACI	
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de	Query Match	99.66	9.99	52.3	51.2	51.2	50.9	50.9	50.8	50.8	20.6	48.9	48.5	48.3	48.2	48.0	48.0	47.9	47.7	47.6	47.5	47.5	47.4	47.3	47.2	47.2	47.1	47.1	46.2	46.0	44.1	43.6	
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# ALIGNMENTS

BRCLD  BRACLD  GEMAT7; GGZZH4;  5-OCT-2004, integrated into UniProtKB)  5-OCT-2004, integrated into UniProtKB)  7-FEB-2006, entry version 15.  hcH (ABC transporter)  ame=yhcH; OrderediocusNames=BL03183, enterilus licheniferais (gtrain DSM 13, dacteria; Pirmicutes; Bacillales; Bacillus licheniferais (gtrain DSM 13, dacteria; Pirmicutes; Bacules; Schenk, Gottschalk, G.; Henne A., id. hrenzeich A., Gottschalk, G.; Henne A., id. hrenzeich A., Gottschalk, G.; Henne A., id. hrenzeich A., Gottschalk, G.; Henne A., Hollomicutes; Bacyllus and compactes of Bacillus arganism-wetth-Great industrians argan T.S., Sorckin A., Bachara, Backang M., Lopez de Leon A., Xiang H., Gottschalk, G.; Barkangsen M.D., Andersen J. arrien T.S., Sorckin A., Bolotin A., Landlich S., D., Berka R.M.; Complete genome sequence of the industrian and comparisons with close and comparisons with close and comparisons and comparisons with close and bolonger (gotton) and comparisons activity; IGA.  Oyyrighted under the Creative Commons stributed under the Creative Commons Science (gotton) (got	1580). Bacillus.	Maurer K.H., H., Merkl R., eniformis DSM13, an	S-10-r77, ody-Karpin S.D., Zaretsky B.J., ody-Karpin S.D., Zaretsky B.J., J.T., Joergensen I.G., J.T., Joergensen P.L., Lapidus A., Galleron N., strial bacterium Bacillus species.", O77.12(2004).	Attribution-Noberive License DNA. DNA. EA.  KNOWN 1.  ide-binding, Transport.
ULT 1  065837_BACLD  065837_BACLD  065837_BACLD  25-OCT-2004, 25-OCT-2	PRELIMINARY; PRT; 307 AA. integrated into UniProtKB/TrEMBL. sequence version 1. entry version 15. naporter). derediocusNames=BL03183, BL100969; enfformis (strain DSM 13 / ATCC 16 micutes; Bacillales; Bacillaceae; '9010;	SEQUENCE [LARGE SCALE GENOMIC DNA]. 1718; DOI=10.1159/000079829; 172berg C., Steckel S., Feesche J., 2., Bacumer S., Henne A., Liesegang 1., Gottschalk G.; 1. Gottschalk G.; 1. Getschalk G.; 1. Gottschal Potential."; 1. Steat industrial Potential."; 1. Obiol. Biotechnol. 7:204-211(2004).	BEQUENCE [LARGE SCALE GENOMIC DNA].  803, DOI=10.1186/gb-2004-5-10-r77; mmaiya P., Nelson B.A., Brody-Karpin ez de Leon A., Kiang H., Gusti V., Rasmussen M.D., Andersen J.T., Joer Sorokin A., Bolotin A., Lapidus A., Berka R.M.; mome sequence of the industrial bac s and comparisons with closely rela 5.RESEARCHO77.1-RESEARCHO77.12(200 TY: Belongs to the ABC transporter	'8 '0'0' 4' B+0'0'
0.	SM3	NUCLECTIDE ( PubMed=1538: Veith B., H( Shrenreich   Ehrenreich   "The complet" Organism wH( ')" Mol. Mic.	NUCLECTIDE & PubMed=1546; PubMe	EMBL; ACD010 EMBL; ACD010 EMBL; CP0010 GO; GO:0005 GO; GO:0006 GO; GO:0006 InterPro; II InterPro; II Pfam; PF0000 Probom; PD00 Probom; PD00 PROSITE; PS0 PROSITE; PS0 ATP-binding;

Length 307;

99.9%; Score 1540; DB 2;

Query Match

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RESULT 3
QBEQIS OCEIH
1D OBEQIS_OCEIH PRELIMINARY; PRT; 307 AA.
AC QBEQIS;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
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EMBL; Z99108; CAB12736.1; -; Genomic_DNA.
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Matches 200; Conservative 4
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=168;
  1e-78;
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MEDLINE=97124185; PubMed=8969498;
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Matches 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical ABC transporter ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RenomeReviews, AL009126 GR; BSU09080.

Subtilist; BG11586; yhcH.

BioCyc; BSUB1423: BSU0908-MONOMER; -.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR003593; AAA_ATPase.

ProDom, P000006; ABC_transp_like.

ProDom, P000006; ABC_transp_like.

Renosite; PS50893; ABC_TRANSPORTER 1; 1.

PROSITE; PS50893; ABC_TRANSPORTER 2; 1.

ATP-binding; Complete protecome; Hypothetical protein; Nucleotide-binding; Transport 1: 305 Hypothetical ABC transporter 1: 305 Hypothetical ABC transporter 2: 4 ATP-binding; Complete protecome; Hypothetical ABC transporter 3: 4 ATP-binding; Complete Droteome; Hypothetical Drotein; ABC Transporter 5: 4 ATP-binding; Complete Droteome; Hypothetical Droteom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997).
--- SIMILARITY: Belongs to the ABC transporter family.
--- SIMILARITY: Contains 1 ABC transporter domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 AA; 34470 MW; 1EBD2DC410BFFB7F CRC64;
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/FTid=PRO 0000093143.
ABC transporter.
ATP (Potential).
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CGVSVKENPEKAARHIGAIVENPELYKPLTGYQNLQQYARMT-KGVTKKKIDEIVELVGL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 GMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPAR-DEKKRYYIQADDTQALTRE 241
                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S VVKLENVRKKIGGTEIIRGLSFEVREGEVYGFLGPNGSGKTTTIRMMTGLISMTEGDITI
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19-JUL-2004, sequence version 1.
19-JUL-2004, sequence version 1.
07-FBB-2006, entry version 14.
ABC transporter, APP-binding protein; possible multidrug transporter.
Name=bcrA; OrderedLocusNames=BT9727 1246;
Bacillus thuringiensis subsp. konkukian.
Bacteria; Firmicutes; Bacillales; Bacillus;
Bacillus cereus group.
NCBI_TAXID=180856;
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                                                                                                                                 Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka I Richardson P., Rubin B., Tice H.; "Complete genome sequence of Bacillus anthracis Sterne."; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Nucleotide-binding; Transport.
SEQUENCE 300 AA; 33378 WW; 4FB1A80D19ACD92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.2%; Score 789; DB 2;
53.7%; Pred. No. 1.5e-36;
iive 59; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                              EMBL; AE017225; AAT53594.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016897; F:ATPasse activity; IEA.
GO; GO:0000166; F:nuclectide binding; IEA.
GO; GO:0000166; P:nuclectide binding; IEA.
GO; GO:0000169; P:transport; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; AAC_transp_like.
Pfam; PF000005; ABC_transporter; 1.
Probom; PD000056; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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QEHLJO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.77
Matches 160; Conservative
                        Bacillus cereus group.
                                                                                                                STRAIN=Sterne;
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LELKNVSKTIRGKKIIEGLSPDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC
                                                                                                                                                       [1]

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=HTEB31 / DSM 14371 / JCM 11309;

MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;

Takami H., Takaki Y., Uchiyama I.;

"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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                                                                                      Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00211; AEC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete proteome; Nucleotide-binding; Trs SEQUENCE 307 AA; 34261 WW; CDPBBF0029C2F5B CRG64;
                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.3%; Score 806; DB 2; 51.3%; Pred. No. 1.7e-37; ive 71; Mismatches 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFIII7_BACAN PRELIMINARY; PRT; 300 AA. 061117_10-101.2004, integrated into UniProtKB/TrEMBL. 19-JUL-2004, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BA000028; BAC13670.1; -; Genomic_DNA.
BioCyc; OIHB182710:0B1714-MONOMER; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BicCyc; OIHE182710; OBLILL-TELLING GO; GO: 0005524; F.ATP binding; IEA.
GO; GO:0005524; F.ATP binding; IEA.
GO; GO:0005524; F.ATP binding; IEA.
GO; GO:000166; F:NUCleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR00353; AAA ATPase.
InterPro; IPR00353; AAA ATPase.
R R TREAPTO; IPR003433; AAC transporter; I.
ProDom; PD000006; ACC transporter; I.
R ProDom; PD000006; ACC transporter; I.
SWART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 30:3927-3935(2002)
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OrderedLocusNames=BAS1274;
                21-FEB-2006, entry version 27.
ABC transporter ATP-binding protein.
OrderedLocusNames=OB1714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2006, entry version 12.
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                                                                                                                                    NCBI_TaxID=182710;
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Gaps

10;

Length 300; 69; Indels 63 64

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64 CGVSVKENPEKAARHIGAIVENPELYKFLTGYQNLQQYARMT-KGVTKKKIDEIVELVGL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 GMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPAR-DEKKRYYIQADDTQALTRE 241
                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 -KANEIIKGKAQRNVIVVSVTKEEIPQLVKKLVNEDVLVYGVTVQNKTLEDEFLAIT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VVKLENVRKKIGGTEIIRGLSFEVREGEVYGFLGPNGSGKTTTIRMMTGLISMTEGDITI
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PubMed=14960714; DOI=10.1093/nar/gkh258;

Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F.,

Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXOl.";

Nucleic Acids Res. 32:977-988(2004).

-I. SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                  which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 300;
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Bacteria, Firmicutes; Bacillales; Bacillus cereus group.
NCBI_TaxIb=222523;
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDB whole genome shotgun (WGS) entry w preliminary data.
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Nucleotidahiding; Transport.
SEQUENCE 300 AA; 33506 MW; E0BIID19DB91DC53 CRC64;
                                                                                                                                                                                                        EMBL, AAEKO1000009; EAL15130.1; -; Genomic_DNA. GO; GO:000524; F:ATP binding; IEA. GO; GO:000581; F:ATP binding; IEA. GO; GO:000166; F:nuclectide binding; IEA. GO; GO:0006810; P:transport; IEA. InterPro; IPR003593; AAA ATPase. InterPro; IPR003439; AAA ATPase. Feam; PF00005; ABC_tran; 1. ProDom; PD0000065, ABC_transporter; 1. ProDom; PD00000606; ABC_transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , DB 2;
2.5e-36;
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50.9%; Score 785; DB
Best Local Similarity 53.9%; Pred. No. 2.5e
Matches 160; Conservative 55; Mismatches
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07-FEB-2006, entry version 12.
ABC transporter, ATP-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
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       Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka : Richardson P., Rubin B., Tice H.; "Complete genome sequence of Bacillus thuringiensis 97-27."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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02-AUG-2005, sequence version 1.
07-FEB-2006, entry version 1.
07-FEB-2006, entry version 1.
Bacitracin transport ATP-binding protein bcrA.
ORFNames=BCE G9241 1172;
Bacillus cereus G9241.
Bactelia; Firmicutes; Bacillales; Bacillus cereus group.
NCBI_TaxID=269801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0211; ABC_TRANSPORTER 1; UNKNOWN_1.
PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete_proteome; Nucleotide-binding; TrissEQUENCE 300 AA; 33378 MW; 4FBIA80D719ACD92 CRC64;

    -I- SIMILARITY: Belongs to the ABC transporter family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.2%; Score 789; DB 2; Best Local Similarity 53.7%; Pred. No. 1.5e-36; Matches 160; Conservative 59; Mismatches 69;
                                                                                                                                                                                     EMBL; AE01355; AAT59400.1; Genomic_DNA.
GO; GO:000554; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0006810; P:Uransport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transp_like.
Fram; PR00005; ABC_transp_like.
Probom; PD00005; ABC_transp_like.
Probom; PD000056; ABC_transporter; 1.
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PubMed=15155910; DOI=10.1073/pnas.0402414101;
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NUCLEOTIDE SEQUENCE.
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Q4MSI37
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Bacillus cereus group.
NCBI TaxID=288681;
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Q63E15;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                       Gaps
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"Comparative genome analysis of Bacillus cereus group genomes with Bacillus subtilis.";

Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.

-I-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                             Length 300;
                                                                                                                                                                                                                                       69; Indels
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Bacillus thuringiensis serovar israelensis ATCC 35646.
Bacillus transcutes; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
NCBI_TaxID=339854;
                                                                                                                                              PROSITE; PS00211; ABC TRANSPORTER 1; UNKNOWN 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
ATP-binding; Complete proteome; Nucleotide-binding; Tri
SEQUENCE 300 Aa; 33353 MW; 5941DAE7B78DD7A7 CRC64;
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                                                                                                                                                                                                              50.9%; Score 785; DB 2; 53.4%; Pred. No. 2.5e-36;
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Bacitracin transport ATP-binding protein bcrA.
                                EMBL; AE017194; AAS40404.1; -; Genomic_DNA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0010869; F:ATP binding; IEA.
GO; GO:0010166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA ATPase.
Fam; PF00005; ABC_transp_like.
PF00005; ABC_transil.
ProDom; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
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Best Local Similarity 53.4*
Matches 159; Conservative
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25-OCT-2004, sequence version 1.
07-FBB-2006, entry version 13.
ABC transporter, ATP-binding protein; possible multidrug transporter.
Name-bCTA; OrderedLocusNames-BCE33111248;
Bacillus cereus (atrain ZR, F331).
Bacillus cereus (atrain ZR, F331).
Bacillus;
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.8%; Score 78%; DB 2; Length 300; 53.4%; Pred. No. 2.9e-36; ive 58; Mismatches 71; Indels
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                    GO, GO: 0005524; F: ATP binding; IEA.
GO; GO: 0016887; F: ATPase activity; IEA.
GO; GO: 000166; F: nucleotide binding; IEA.
GO; GO: 000610; P: transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transp_like.
Fram; PF00005; ABC transp_like.
Probom; PD000005; ABC transporter; 1.
PROSITE; PS00931; ABC TRANSPORTER 1; UNKNOWN 1.
PROSITE; PS06993; ABC TRANSPORTER 2; 1.
ATP-binding; Nucleotide-binding; Transport.
SEQUENCE 300 AA; 33369 MW; 841D6E496F197457 CR
EMBL; AAJM01000404; EAO52546.1; -; Genomic_
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003499; ABC_transp_like.
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Matches 159; Conservative 5
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STRAIN=97-27;
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QEHANS;
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                                                                                                                                                                                                                                                                                               4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
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MEDLINE-22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Gacchkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.C.;
"Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                    9
                                                                                                                          Transport
                                                                                                                                                                                              Length 300;
                                                                                                                                                                                                                                                 75; Indels
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01-JUN-2003, sequence version 1.
07-FEBE-2006, entry version 16.
Bacitracin transport ATP-binding protein bcrA.
OrderedLocusNames=BC1359; ORFNames=BC 1359;
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacieria, Firmicutes; Bacillales; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 423:87-91(2003).
-!- SIMILARITY: Belongs to the ABC transporter family.
Pfam; PF00005; ABC_tran; 1.

ProDour; PD00006; ABC_transporter; 1.

SWART; SR00382; AAA; 1.

PROSITE; PS00211; AAG_TRANSPORTER_1; UNKNOWN_1.

PROSITE; PS0023; ABC_TRANSPORTER_1; UNKNOWN_1.

ATP-binding; Complete Compose one; Nucleotide-binding; Tri

SEQUENCE 300 AA; 33561 WW; 14P4E9A8CA306D53 CRC64;
                                                                                                                                                                                                 50.8%; Score 783; DB 2; 53.9%; Pred. No. 3.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
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BioCyc; BCER226900:BC1359-WOWGRER, -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR00349; ABC_transp_like.
ProDom: PP00006; ABC_tran; I.
SWART; SM0382; AAA; I.
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Q81GS1;
                                                                                                                                                                                                                          Best Local Similarity 53.9
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus anthracis.",
Nature 423:87-91(2003)
                                                                                                                                                                                              Query Match
Best Local Similarity
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64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMT-KGVTKKKIDEIVELVGL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 KORINDKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREK 182
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                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                         4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                     5 VVKLENVRKKIGGTEIIRGLSFEVREGEVYGFLGPNGSGKTTTIRMMTGLISMTEGDITI
                                                                                                                                                                               Gaps
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07-FEB-2006, entry version 14.
ABC transporter, AFP-binding protein; possible bacitracin transport
ATP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka Stichardson P., Rubin E., Tice H., "Complete genome sequence of Bacillus thuringiensis 97-27.", Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  10;
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34326 MW; 92E123A0CBC4DDD7 CRC64;
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete_proteome; Nucleotide-binding; Transport.
SEQUENCE 300 AA; 33300 MW, BFC416D41D47E21B CRC64;
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                                                                                                                    50.6%; Score 781; DB 2; Length 300;
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Bacillus thuringiensis subsp. konkukian.
Bacteria; Firmicutes; Bacillales; Bacillus;
Bacillus cereus group.
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48.2%; Pred. No. 1.3e-34;
                                                                                                                                                   4.2e-36;
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PROSITE; PS00211; ABC TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC TRANSPORTER_2; 1.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016891; F:ATPase activity; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; ABC_transp_like.
Pfam; PF00005; ABC_tran; I.
SMAPT. SMO1382. AAA. 1
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                                                                                                                                             53.4%; Preu. ...
tive 57; Mismatches
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                                                                                                                       Query Match
Best Local Similarity 53.44
Matches 159; Conservative
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SEQUENCE 305 AA; 34
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EMBL/GenBank/DDBJ databases.
      ubmitted (MAY-2004) to the EMBL/GenBank/DDBJ database:
|- SIMILARITY: Belongs to the ABC transporter family.
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Q3EW61;
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NCBI_TaxID=339854;
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TIGR; I
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X NUCLECLIES SUCKNET LINEAGES OCALES SERVICED UNITS.

A READ T.D., Peterson S.N., Tourasse N.J., Baillat L.W., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., W.M.,

A KOlonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Redmond C., Thwaite J.E., White O.,

Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

The genome sequence of Bacillus anthracis Ames and comparison to

closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LETLLELKNVSKTIRGKKI I EGLSFDVRAGEI FGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                           121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
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                                                                                                                                                                                         61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
      Gapa
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kinaka R.,
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   17;
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QBIJQ2; Q6HQ9B;
QBIJQ2; Q6HQ9B;
QBIJQ2; Q6HQ9B;
QBIJQA-2003, integrated into UniProtKB/TrEMBL.
Q1-UNA-2003, sequence version 1.
O7-FEB-2006, entry version 20.
ABC transporter, ATP-binding protein.
OrderedLocusMames=BAS650, BAS5252, GBAAS650; ORFNames=BA_5650;
   76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
Bacillus cereus group.
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69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRFLEITADKEEA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLFIELTRGEOHA 305
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Ames ancestor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1392;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 EAAAFRKVKVDEAEGGIELSIQKD-----EVPDLIKHLTDSGVRLYEVKAVNKSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 35646;
Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,
Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete proteones; Nucleotide-binding; Transport.
SEQUENCE 305 AA; 34399 WW; 641282488BA6C24A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.2%; Score 748.5; DB 2; Deliyer. 48.2%; Pred. No. 2.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2005, integrated into UniProtKB/TrEMBL.
08-NOV-2005, sequence version 1.
07-FRB-2006, entry version 4.
Bacitracin transport ATP-binding protein bcrA.
ORPNameseRBH 05356,
Bacillus thuringiensis serovar israelensis ATCC 35646.
Bacillus firmicutes; Bacillaceae; Bacillus;
                                                                                                                                                                                       EMBL; AE016879; AAP29284.1; -; Genomic DNA.
EMBL; AE017225; AAT57540.1; -; Genomic DNA.
EMBL; AE017334; AAT70166.1; -; Genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; GBAA5650; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0000166; F:RUPGlectide binding; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA ATPase.
InterPro; IRR003439; ABC_transp_like.
Pfam; PF00005; ABC_tran; I.
ProDom; PD000066; ABC_transporter; I.
SWART; SW00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 EKGMAVIVSSHLLSEMELMCDRIAJIQNGKLRDIQHVHGPARDEKKRY-YIQADDTQALT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :::|| :::|| ::|| | ::|
-----KDMLEDAEEVREVSIEGDRLLCRMNIASISNWNKHFVENEIDVHSVKELVFTL 291
                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 REAAAFRKVKVDEAEGGIELSIQKD-----EVPDLIKHLTDSGVRLYEVKAVNKSL
                              PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
Shores K.A., Fouts D.E., Tourase N.J., Angluoli S.V., Kolonay J.F.,
Nelson W.C., Kolstce A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
adapterions and a large plasmid related to Bacillus anthracis pXOl.";
Nucleic Acids Res. 32:977-988(2004).
-: SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0211; ABC_TRANSPORTER_1; UNKNOWN_1.
PROSITE; PSG0893; ABC_TRANSPORTER_2; ATP-binding; Transport.
ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SEQUENCE 305 AA; 34406 MW; FDEEA942EIDFF99A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.2%; Score 743.5; DB 2; Length 305; 47.8%; Pred. No. 5.5e-34; ive 68; Mismatches 77; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus,
   SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AE017194; AAS44429.1; -; Genomic_DNA.GO; GO:0005524; F:ATP binding; IEA.GO; GO:001689; F:ATP binding; IEA.GO; GO:000166; F:nucleotide binding; IEA.InterPro; IPR003593; AAA_ATPase. InterPro; IPR003439; ABC_transp_like.Pfam; PF00005; ABC_transp_like.ProDom; PD000006; ABC_transp_like.ProDom; SNART; SN00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2005, sequence version 1.
07-FEB-2006, entry version 7.
Bacitracin transport ATP-binding protein borA.
Prepames-EDE G2241 5584;
Bacillus cereus G9241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=G9241;
PubMed=15155910; DOI=10.1073/pnas.0402414101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q4MLR2_BACCE PRELIMINARY;
Q4MLR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDLFIELTRGEQHA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDRFLEITADKEEA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 47.8
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus cereus group.
NCBI_TaxID=269801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 MLEAAEEVREVSVE----GERLLCRMDIASISSWNKHLVENEIDVHSVKELVFTLEDLFI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDBPTNGLDPAGIREIRDYLRKLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKGMAVIVSSHLLSEMELMCDRIALIQNGKL---RDIQHVHGPARDEKKRYYIQADDTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 BENMSVFISSHLLSEVQMICDRVAIIHKGKMITVAKVEELIKTASDRVEWIVTPISKAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Goltsman E., Chu L., Fonstein M., Ehrlich D., Overbeek R., Kyrpides N., Ivanova N.;
"Comparative genome analysis of Bacillus cereus group genomes with Bacillus subtilis.";
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-!- SIMILARITY: Belongs to the ABC transporter family.
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Bacillus cereus (strain ATCC 10987).
Bacicria; Firmicutes; Bacillales; Bacillus;
Bacillus cereus group.
NCBI_TaxID=222523;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AAJM01000065; EAOS5544.1; -; Genomic_DNA.GO; GO:0005524; F:ATP binding; IEA.GO; GO:0016897; F:ATPabea activity; IEA.GO; GO:000166; F:ATPabea activity; IEA.GO; GO:0000166; F:ATPabea activity; IEA.INTERPRO; IPRO0393; AAA_ATPabea.InterPro; IPRO03043; ABC transplike.InterPro; IPRO02048; EF_Band_Ca_bd. Probom; PD000005; ABC transplike.Probom; PD0000065; ABC transporter; 1.SM0382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 48.3%; Score 744.5; DB 2; Local Similarity 47.9%; Pred. No. 4.8e-34; Hes 148; Conservative 70; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO0211; ABC_TRANSPORTER 1; UNKNOWN 1. PROSITE; PS50893; ABC_TRANSPORTER 2; 1. PROSITE; PS001018; EF HAND 1; UNKNOWN 1. PROSITE; PS001018; EF HAND 1; UNKNOWN 1. SEQUENCE 305 AA; 34330 WW; CASO06F148498EEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 AA
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07-FRB-2006, entry version 13.
ARC transporter, ATP-binding protein.
ORFNames-ERCE_5529;
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EKGMAVIVSSHLLSEMELMCDRIALIQNGKL---RDIQHVHGPARDEKKRYYIQADDTQA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D., Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W., Maiden M.C.J., Priest P.G., Barker M., Jiang L., Cer R.Z., Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D., Popovic T., Fraser C.M.; Weyant R.S., Galloway D.R., Read T.D., Popovic T., Fraser C.M.; indeprivation of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax."; Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-I. CAVIION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
-I. SIMILARITY: Belongs to the ABC transporter family.
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Best Local Similarity 47.6%; Pred. No. 9.2e-34;
Matches 147; Conservative 68; Mismatches 85; Indels 9
                                                                                                                                                                                                                                                                                   REMBL, AAEKKOLO0030, EALJ3109-11, -;

REMBL, AAEKKOLO00030, EALJ3109-11, -;

R GO; GO:0005524; F:ATPase activity, IEA.

R GO; GO:000166; F:nuclectide binding; IEA.

R GO; GO:000160; P:ransport; IEA.

R InterPro; IPR003593, AAA ATPASE.

R InterPro; IPR003593, ABC transport; IEA.

R PRODOM; PD000006; ABC transporter; 1.

R PRODOM; PD000006; ABC transporter; 1.

R PROSITE; PS00301; ABC TRANSPORTER 1; UNKNOWN 1.

R PROSITE; PS00018; EF HAND 1; UNKNOWN 1.
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Search completed: July 13, 2006, 13:49:00 Job time : 301 secs

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GenCore version 5.1.9
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- protein search, using sw model OM protein

July 13, 2006, 13:49:18 ; Search time 50 Seconds (without alignments) 537.438 Million cell updates/sec Run on:

US-10-510-941-2 1542 1 LETLLELKOVSKTIRGKKII.......KSLEDRFLEITADKEEAQHV 307 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

650591 segs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/R\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/R\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/R\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		P				
Result		Query				
No.	Score	Match	Match Length	DB	ID	Description
-	455.5	29.5	310	7	US-09-107-532A-6910	Sequence 6910, Ap
7	436	28.3	233	~	US-09-627-376-12	
m	436	28.3	233	~	US-10-047-676B-12	12,
4	430.5	27.9	332	~	US-09-107-532A-3752	٠.
S	416.5	27.0	303	7	US-09-107-532A-5192	
y	410	26.6	345	~	US-09-252-991A-31957	
7	408.5	26.5	330	~	US-09-902-540-15345	
8	407.5	26.4	319	~	US-09-758-759-89	
6	397	25.7	328	~	US-09-902-540-10796	
10	396.5	25.7	309	7	US-09-252-991A-21204	
11	392.5	25.5	215	~	US-09-583-110-2846	
12	392.5	25.5	229	7	US-09-107-433-3116	٠.
13	391.5	25.4	309	7	US-09-902-540-16586	
14	384.5	24.9	228	~	US-09-602-787A-402	
15	381	24.7	788	N	US-09-252-991A-28171	
16	374.5	24.3	240	~	US-09-902-540-15786	
17	373	24.2	292	~	US-09-602-787A-352	Seguence 352, App
18	371.5	24.1	290	7	US-09-902-540-16248	
19	371.5	24.1	594	~	US-09-543-681A-5528	Sequence 5528, Ap
20	367	23.8	588	7	US-09-489-039A-13579	13579,
21	363.5	23.6	315	~	US-09-134-000C-6449	_
22	362.5	23.5	245	8	US-09-902-540-13001	13001,
23	354.5	23.0	248	~	US-09-710-279-3218	٠.
24	352.5	22.9	316	7	US-09-902-540-10994	10994
25	349.5	22.7	1272	7	US-09-949-016-7472	Sequence 7472, Ap
56	347.5	22.5	2059	ო	US-10-114-270-176	Sequence 176, App

NAME/KEY: misc feature LOCATION: (B) LOCATION 1...310 SEQUENCE DESCRIPTION: SEQ ID NO: 6910:

FEATURE

Sequence 2, Appli Sequence 6947, Ap Sequence 25, Appl	Sequence 25, Appl Sequence 75, Appl Sequence 120, Appl Sequence 10796, A	Sequence 5424, Ap Sequence 18351, A Sequence 4066, Ap Sequence 4766, Ap	Sequence Sequence Sequence Sequence	Sequence 5279, Ap Sequence 3331, Ap Sequence 4388, Ap Sequence 3, Appli
US-10-154-419-2 US-09-949-016-6947 US-08-665-259-25	US-08-762-500-25 US-08-762-500-75 US-09-032-438C-120 US-09-949-016-10796	US-09-107-532A-5424 US-09-252-991A-18351 US-09-107-532A-4066 US-09-134-001C-4766	US-09-107-532A-4983 US-09-107-532A-4205 US-09-489-039A-12496 US-09-328-352-7592	US-09-583-110-5279 US-09-107-433-3331 US-09-328-352-4388 US-09-032-438C-3
2144 2 2146 2 1684 2	1684 2 1704 2 1704 2 1766 2	304 607 257 205 205	254 323 323 589 222 223 223 223 233 233 233 233 233 23	317 2 327 2 315 2 2273 2
2225	22.5 22.5 22.5 25.5 25.5	2222 2223.4 4.6.6.5	22.0 22.1 22.0	22.0 22.0 21.7 21.7
347.5 347.5 346.5	346.5 346.5 346.5	345.5 344.5 344	341.5 341 340 339.5	339 334 334.5
22 28 29 80	33 33 33 33 33	4 8 8 8 4 8 4 8 9 4 8 9 9 9 9 9 9 9 9 9	38 39 40 41	4 4 4 4 6 6 4 7

## ALIGNMENTS

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Sequence 6910, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC

OPERATING SYSTEM: «UNKNOWN:
SOFTWARE: ASCIT

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinfello, Pamela Deneke
REGISTRATION NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (781)893-507
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6910:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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RESULT 1
US-09-107-532A-6910
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Best Local Similarity
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                                                                                                                               Indels
                                              Query Match 28.3%; Score 436; DB 2; Best Local Similarity 41.5%; Pred. No. 3.7e-34; Matches 93; Conservative 51; Mismatches 72.
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Sequence 12, Application US/09627376

Patent No. 6342365

GENERAL INFORMATION:
APPLICANT: Q1, Fengxia
FILE OF INVENTION: MTTACIN I BIOSYNTHESIS GENI
FILE REFERENCE: UAB-17402/22

CURRENT PAPLICATION NUMBER: US/09/627,376

CURRENT PILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12

SEQ ID NO 12
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                                                                                                                               Matches 104; Conservative
                                                               Query Match
Best Local Similarity
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US-09-107-532A-6910
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US-10-047-676B-12
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Sequence 12, Application US/10047676B

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RESULT 4
US-09-107-532A-3752
i Sequence 3752, Application US/09107532A
j Sequence 3752, Application US/09107532A
j Patent No. 6583275
j GENERAL INFORMATION:
j TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
j TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
GREATAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Qi, Fengala
APPLICANT: Canfield, Page W.
APPLICANT: Chen, Ping
TILLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
FILE REFERENCE: UAB-17403/22
CURRENT APPLICATION NUMBER: US/10/047,676B
CURRENT FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 09/627,376
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 19
SOFFWARE: Patentin version 3.2
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 28.3%; Score 436; DB 2; Length 233; 1 Similarity 41.5%; Pred. No. 3.7e-34; 93; Conservative 51; Mismatches 72: TnAn a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDE 224
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/09/107,532A
FILING APPLICATION NUMBER: 00/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Affiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40.489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus mutans
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Sequence 31957, Application US/09252991A

Sequence 31957, Application US/09252991A

Sequence 31957, Application US/09252991A

GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31957

LENGTH: 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 AVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDIQALTREAAA 244
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-6277
INFORMATION FOR SEQ ID NO: 5192:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               )

NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...303

SEQUENCE DESCRIPTION: SEQ ID NO: 5192:
US-09-107-532A-5192
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 CGVSVKENFEKAARHIGAIVENPELYKFLIGYONL---QQYARMTKGVTKKKIDEIVELV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 Q--TTILFSTHILSDVVRICDKVAFLDNGKI-----VLSGSVDELKK------QTNASGF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAAAFRKVKVDEAE----GGI---ELSI----OKDEVPDLIKHLTDSGVRLYEVKAVNK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 EIVFFSKKEREOFEELLPGGMIRSELRIAYPQKSKEEMLFAMDLLAKYOLPVOSVQMEEP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.9%; Score 430.5; DB 2; Length 332; Best Local Similarity 35.9%; Pred. No. 2.1e-33; Matches 111; Conservative 60; Mismatches 109; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           ;
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...332
;
SEQUENCE DESCRIPTION: SEQ ID NO: 3752:
US-09-107-532A-3752
                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/085,598
                   TELEPHONE: (781)893-5007
TELEFAX: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3752:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: mino acids
TYPE: TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5192, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 TĽEKLFĽEV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 SLEDRFLEI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-107-532A-5192
                                                                                                                                                                                                                                                                                            FEATURE
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56 ITAGEIAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTK----K 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 KIDEIVELVGLKANRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 RDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 ADDTQALTREAAAFRK----VKVDEAEGGIELSIQKDE----VPDLIKHLTDSGVRLYE 282
                    224 EKKRYYIQADDTQALTREAAAFRKVKVDEAEGGIELSIQKDE--VPDLIKHLTDSGVRLY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10736, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:
APPLICANT: Glodman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Seeven C.
APPLICANT: Slater, Seeven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LLELKNVSKTIRGK-----KIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMS
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26.4%; Score 407.5; DB 2; Length
Best Local Similarity 32.0%; Pred. No. 3.4e-31;
Matches 101; Conservative 65; Mismatches 125; Indele
                                                                                                                                                                                                                                                                                                                                                                        Sequence 89, Application US/09758759;
Patent No. 6861513;
GENERAL INFORMATION:
APPLICANT: HOSTEN, Time X.
TITLE OF INVENTION: Everiniomaicin Biosynthetic Genes
TITLE OF INVENTION: Everiniomaicin Biosynthetic Genes
TITLE OF INVENTION: Everiniomaicin Biosynthetic Genes
TITLE OF INVENTION NUMBER: US/09/758,759
CURRENT FILING DATE: 2001-01-11
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Micromonospora carbonacea
                                                                                                                                                                                                                          295 SVALRRPTLADVFLQLT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 VKAVNKSLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 IELHRPSLDDVFLTKT 312
                                                                                                                                                           282 EVKAVNKSLEDRFLEIT
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US-09-758-759-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-902-540-10796
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US-09-758-759-89
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Patent No. 683347

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hiseand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 15345
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                                                                                                                                                                                                                                                                                                                                                             62 AVCGVSVKENFEKAARHIGAIVENPELY-----KFLTGYQNLQQYARMTKGVTKKKIDE 115
                                                                                                                                                                                                                                                                                                                                                                                                          116 IVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYL 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 RKLTREKGMAVIVSSHLLSEMELMCDRIAJIQNGKLRDIQHVHGPARDEKKRYYIQADDT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | | : : | | |: BAPUDPLAIAMLPGVAGIEGRPDRAGILTILARPGVQI-----LPALNRLIHGSGWRVS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AVCGVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGV----TKKKIDEIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 ELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKL------RDIQHVHGPARD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 LRDSEGLTVLLTTHRADEAD-VCDRLAVLDAGKLVACDTPQALASRMGGDILSV---- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 QALTREAAAFRKVKVDEAEG------GIELSIQKDEVPDLIKHLTDSGVRLY 281
                                                                                                                                                                                                                                                                   213 KNLSESK--IVVISTHILEEVSFMCSRALVINGGRLL-ADNTPGELRTRSRYHHAVSLSI
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                                                                                                                                                                                                                          2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI
                                                                                                                                                                  Gaps
                                                                                                                                                                  32;
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                                                                                                Length 345
                                                                                             Query Match 26.6%; Score 410; DB 2; Length 34: Best Local Similarity 29.5%; Pred. No. 2.2e-31; Matches 94; Conservative 77; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.5%; Score 408.5; DB 2; Best Local Similarity 31.5%; Pred. No. 2.9e-31; Matches 100; Conservative 71; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 GVRTEHGOLEEVFROLTRE 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 EVKAVNKSLEDRFLEITAD 300
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-902-540-15345
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Sequence 2846, Application US/09583110

Sequence 2846, Application US/09583110

Batent No. 6659703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcu

ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcu

ITILE OF INVENTION: NUMBER: US 09/107,433

FILE REFERENCE: PATE: 2000-08-26

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322
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                                               KKIDEIVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIRE 170
                                                                                  122 LELDEV------RQTIETLSKGFRRVGLAQAILHEFRALVLDEFTDGLDFNQKHQ 172
                                                                                                                                                           227
                                                                                                                                                                                                230 IQADDTQALT-----REAAAF-----RKVKVDEAEGGIELSIQKDEV--PDLIKHLTD 275
                                                                                                                                                                                                                        228 -----QAVTLYSDEPLDAVALAVLPGVAGIEENPAEGSLTVLAQPGAVIFPQVSGLVAE 281
         62 IFGFDIRNRTLQAQRLIGYLPEGSPCYAEMTVQGFLDFIAEIRGYRGAGKRERVARALGL 121
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Patent No. 6800744

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE

HERRAPEUTICS

THERAPEUTICS

THERAPEUTICS
                                                                                                                                             171 IRDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGK-LRDIQHVHGPARDEKKRYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.5%; Score 392.5; DB 2; Best Local Similarity 33.7%; Pred. No. 5.5e-30; Matches 70; Conservative 62; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 EKGMAVIVSSHLLSEMELMCDRIAIION 208
                                                                                                                                                                                                                                                                         276 SGVRLYBVKAVNKSLEDRFLEITADKE 302
                                                                                                                                                                                                                                                                                                 282 RGWRIRELDVERGRLDEVFRNLTRGTE 308
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EKGTTILIASHSEBDIRILCDKVYAIED
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US-09-107-433-3116
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                             120 VGLKONRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :: || | :: :: || 241 VGDAGNAVWERAERVLLEQPRVKRVAREGEALRVRLELDAGAGPAQVDA---AAAVLLAA 297
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                                                                                                                                                                                                                                                                                                                                  180 REKGMAVIVSSHLLSEMELMCDRIAIIQ-----NGKLRDI---QHVHGPARDE----
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                                                                                                                                                                                                                                  Length 328;
                                                                                                                                                                                                                                Query Match 25.7%; Score 397; DB 2; Length 32:
Best Local Similarity 31.0%; Pred. No. 3.7e-30;
Matches 101; Conservative 72; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 25.7%; Score 396.5; DB 2; 1 Similarity 30.0%; Pred. No. 3.8e-30; 98; Conservative 71; Mismatches 111;
FILE REFERENCE: 30-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTDSGVRLYEVKAVNKSLEDRFLEIT 298
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ORGANISM: Pseudomonas aeruginosa
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Best Local S
Matches 98
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Sequence 402, Application US/09602787A

| Sequence 402, Application US/09602787A
| Patent No. 6696561
| GENERAL INFORMATION:
| APPLICANT: Pompedius, Mark
| APPLICANT: Sch'der, Hartwig
| APPLICANT: Sch'der, Hartwig
| APPLICANT: Sch'der, Hartwig
| APPLICANT: Sch'der, Obkar
| TITLE OF INVENTION: CORYNEAGACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
| TITLE OF INVENTION: TRANSPORT |
| TITLE OF INVENTION: TRANSPORT |
| TITLE OF INVENTION: TRANSPORT |
| FILE REFERENCE: BG1-125CP |
| TITLE OF INVENTION: TRANSPORT |
| FILE REFERENCE: BG1-125CP |
| TITLE OF INVENTION: TRANSPORT |
| FILE REFERENCE: BG1-125CP |
| FRIOR FILING DATE: 1999-07-08 |
| PRIOR FILING DATE: 1999-07-09 |
| PRIOR PELICATION NUMBER: DE 1933212.1 |
| PRIOR FILING DATE: 1999-07-09 |
| PRIOR PELICATION NUMBER: DE 1933212.5 |
| PRIOR PELICATION NUMBER: DE 1933212.6 |
| PRIOR FILING DATE: 1999-07-09 |
| PRIOR PELICATION NUMBER: DE 1933212.6 |
| PRIOR PELICATION NUMBER: DE 1933212.6 |
| PRIOR PELICATION NUMBER: DE 1933212.6 |
| PRIOR PELICATION NUMBER: DE 1993212.6 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 KRYYIQADDTQALTREAAAFRKVKVDEAEGG-IELSIQ--KDEVPDLIKHLTDSGVRLYE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 AR-----AVEVLOR----FGSVEVDRASDGLVALTVRASPDORPQVAQAVVGAGLELLR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LLELKAVSKTIRGKKIJEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                             Length 309;
                                                                                                                                                                                                                                                                                                                                             Query Match
25.4%; Score 391.5; DB 2; Length 3
Best Local Similarity 32.8%; Pred. No. 1.2e-29;
Matches 105; Conservative 62; Mismatches 118; Indels
     rITLE OF INVENTION: Myxococcus xanthus Genom
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 VKAVNKSLEDRFLEITADKE 302
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US-09-902-540-16586
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        NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...229
; SEQUENCE DESCRIPTION: SEQ ID NO: 3116:
US-09-107-433-3116
                                                                                                                                                                                                                                                                                                                         SOFTWARE: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 EKGMAVIVSSHLLSEMELMCDRIAIIQN 208
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EKGTTILIASHSEDIRILCDKVYAIED 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3116:
SEQUENCE CHARACTERISTICS:
LENGTH: 229 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781)893-8277
                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                      CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-902-540-16586
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Sequence 28171, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
APPLICANT: Marc 10196.136
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
                                                         121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                             181 EKGMAVIVSSHLLSEMELMCDRIALIQNGKL 211
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he: 52 secs
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 EAQHV 307
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US-09-252-991A-28171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MINVEGLIKQYGQVRAVDDLSFEVKPGIVTGFLGPNGAGKSTTWRLILGLDNPTAGHATI 60
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24.9%; Score 384.5; DB 2;
Best Local Similarity 41.2%; Pred. No. 3.66-29;
Matches 87; Conservative 45; Mismatches 70;
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-04
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-08-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-09-31
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123 KNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREK 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 GMAVIVSSHILSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIA
                                                                                                                                                                                                              63 VCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGL
Length 788;
  Query Match

24.7%; Score 381; DB 2; Length 786

Best Local Similarity 31.8%; Pred. No. 4.9e-28;

Matches 97; Conservative 57; Mismatches 111; Indels
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GTGIVLCSHVLPGVETHIDRAAILAGGRLQ-
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CGV---SVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELV 120 

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Sequence:

Searched:

Database

Result No.

70273710843711088765

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Sequence 1502, Ap
Sequence 10399, A
Sequence 11165, A
Sequence 6521, Ap
Sequence 6521, Ap
Sequence 1202, Ap
Sequence 1771, Ap
Sequence 1771, Ap
Sequence 1771, Ap
Sequence 17789, A
Sequence 1789, A
Sequence 17469, A
Sequence 1768, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR
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                                                                          Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10510941
; Sequence 2, Application US/10510941
; Publication No. US20060040346A1
; GENERAL INFORMATION:
; APPLICANT: JOrgensen, Steen Troels
; APPLICANT: Raemussen, Michael Dolberg
; APPLICANT: Raemussen, Jens Tonne
; APPLICANT: Clesen, Peter Bjarke
; APPLICANT: Clesen, Peter Bjarke
; APPLICANT: Clesen, Deter Bjarke
; APPLICANT: Clesen, Deter Bjarke
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILER REFERENCE: 10297.204-US
; CURRENT APPLICATION NUMBER: US/10/510,941
; CURRENT FILING DATE: 2004-10-08
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO :

LENGTH: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 1542; DB 5; Similarity 100.0%; Pred. No. 6.9e-123; 07; Conservative 0; Mismatches 0;
                      US-10-156-761-10399
US-10-156-761-14601
US-10-36-91-11165
US-09-738-626-6521
US-10-369-493-16655
US-10-369-493-16655
US-10-369-493-1098
US-10-732-923-1771
US-10-732-923-1771
US-10-732-923-1771
US-10-732-923-17783
US-10-369-493-1783
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US-10-369-493-17869
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US-10-369-493-17869
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4 421.5
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Best Local S:
Matches 307,
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Sequence 16618, A
Sequence 60404, A
Sequence 182, App
Sequence 183, App
Sequence 17122, A
Sequence 17122, A
Sequence 17122, A
Sequence 1336, Ap
Sequence 1297, Ap
Sequence 1297, Ap
Sequence 1297, Ap
Sequence 12401, A
Sequence 54022, A
Sequence 54022, A
Sequence 54022, A
Sequence 1559, Ap
Sequence 1259, Ap
Sequence 12, Appl
Sequence 1826, A
                                                                                                                                                            July 13, 2006, 13:49:57 ; Search time 186 Seconds (without alignments) 764.554 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                              US-10-510-941-2
1542
1 LETLLELKNVSKTIRGKKII......KSLEDRFLEITADKEEAQHV 307
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                           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-510-941-2
US-10-369-493-16618
US-10-369-493-16618
US-11-045-004-182
US-11-045-004-182
US-10-369-493-17322
US-10-369-493-17322
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US-10-7732-928-1728-53430
US-10-7732-928-1728-53430
US-10-7732-928-1728-53430
US-10-7732-928-1728-53430
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US-10-7732-928-1728-53430
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US-10-282-122A-52344
US-10-369-493-18115
US-10-369-493-18754
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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COSSART, PASCALE
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US-11-045-004-182
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        Sequence 16618, Application US/10369493
Publication No US20030233675A1
GENERAL INCORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yangwei
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REPRENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT APPLICATION NUMBER: US/60,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16518
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Applicant: Zyskind, Undith
APPLICANT: Olleen, Kari
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoco, Robert
APPLICANT: Yamamoco, Robert
APPLICANT: Yamamoco, Robert
APPLICANT: Porryth, R.
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62 AVCGVSVKENFEKAARHIGAIVENPELYKFLTGYONLOQYARMTKGVTKKKIDEIVELVG 121
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CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR PLING DATE: 2000-03-21
FRIOR PLING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-23
FRIOR PLING DATE: 2000-05-24
FRIOR PLING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-06
FRIOR FILING DATE: 2000-09-09
FRIOR PLING DATE: 2000-09-09
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-2-2
FRIOR FILING DATE: 2000-11-2-2
FRIOR FILING DATE: 2001-12-2
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-04
FRIOR FRIO
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47.6%; Score 734; DB 4; Length 301;
Best Local Similarity 49.8%; Pred. No. 4.8e-54;
Matches 149; Conservative 61; Mismatches 81; Indels
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APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: NCONIOK, CHRISTOPHE
APPLICANT: PSIHI, HAFIDA
APPLICANT: DEHOUX, PIERRE
APPLICANT: CHETOUANI, FARID
APPLICANT: CHETOUANI, FARID
APPLICANT: GLIGABER, PHILIPPE
APPLICANT: GLIASER, PHILIPPE
APPLICANT: GLIASER, PHILIPPE
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US-10-282-122A-60404
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BERCHE, PATRICK
CHARBIT, ALAIN
DURANT, LIONEL
BEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
GARCIA DEL PORTILLO, FRANCISCO
GOMEZ-LOPEZ, NURIA
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DOMINGUEZ-BERNAL, GUSTAVO
GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
                                                            Sequence 885, Application US/11045004
Publication No. US20060078901A1
GENERAL INFORMATION:
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COUTE, ELISABETH
RUSNIOK, CHRISTOPHE
PSIHI, HAPIDA
DENOKY, PIERRE
DUSSURGET, OLIVIER
CHETOUANI, PARID
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PABLOS, BETRIZ DE
WEHLAND, JURGEN
KARST, UWE
ENTIAN, KARL-DIETER
HAUF, JORG
NOSE, MATTHIAS
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CHAKRABORTY, TRINAD
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DANIELS, JUSTIN
GOEBEI, WERNER
KREFT, JURGEN
KUHN, MICHAEL
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GLASER, PHILIPPE
KUNST, FRANCK
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HAIN, THORSTEN
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LENGTH: 306
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BAQUERO, FERNANDO
GARCIA DEL PORTILLO, FRANCISCO
                                                                                                                                       VAZQUEZ-BOLAND, ANTONIO
DOMINGUEZ-BERNAL, GUSTAVO
GARRIDO-GARCIA, PATRICTA
TIERREZ-MARTINEZ, ALBERTO
AMEND, ALEXANDRA
CHAKRABORTY, TRINAD
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; ORGANISM: Listeria monocytogenes
US-11-045-004-182
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KARST, UWE
ENTIAN, KARL-DIETER
HAUF, JORG
ROSE, MATTHIAS
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MADUENIO, ENCARNA
PABLOS, BETRIZ DE
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CHARBIT, ALAIN
DURANT, LIONEL
DANIELS, JUSTIN
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KUHN, MICHAEL
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2 ETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEI 61 TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES CURRENT PRICED APPLICATION NUMBER: 2011/045,004
CURRENT FILING DATE: 2005-01-28
PRIOR FILING DATE: 2005-01-18
PRIOR PLICATION NUMBER: 10/637,023
PRIOR PLICATION NUMBER: PCT/FR01/01118
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR PLING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: FR 00/04,629
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2854
SOPTWARE: PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTING DATE: 2001-04-11 Gaps 7 Query Match 41.4%; Score 639; DB 6; Length 306; Best Local Similarity 45.3%; Pred. No. 6.1e-46; Matches 135; Conservative 57; Mismatches 104; Indels

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184 MAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAA 243
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34.8%; Score 536; DB 4; Length 302;
Best Local Similarity 39.3%; Pred. No. 3.6e-37;
Matches 116; Conservative 64; Mismatches 111; Indels
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Streptococcus mutans US-10-282-122A-72352
                                Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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185 AVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARD-EKKRYYI----QADDTQALT 239
                                                                                   GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                          123 KLTGAINQKVKTYSLGMRQRLGVAQALIHSPALLILDEPTNGLDPQGMAEFRTLIRDLA- 181
                                                                                                                                                                  181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240
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                                                                                                                                                                                             5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
                                                                                                                                                                                                                                                                          242 VLATLPVKLVAQNEDLFKIEVAHEDVHLIARALIQANIDLLEMVPLQASLEERFLELT 299
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44.0%; Pred. No. 7.5e-46;
tive 66; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 84, Application US/10510386
PUblication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Clausen, Recen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFRENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: Patentin version 3.3
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; Sequence 72352, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Mang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Bacillus licheniformis US-10-510-386-84
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION C
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5205.2)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20363
                                                      80 VGSLIESPSYYGHLSGYENLRIIATL-KGTPEKDIGRVLEIVRLENQKNKKTNQYSLGMK 138
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                                                                                                                                            199 MCDRIAIIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTREAAAFRKVKVDEAEGGIE 258
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                            79 IGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIVELVGLKNRINDKVKTYSLGMR
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Sequence 20363, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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US-10-369-493-1297
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Alater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (22052)8
CURRENT APPLICATION NUMBER: US 60/360,039
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR APPLICATION NUMBER: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9838
LENGTH: 299
                                                                         g
APPLICANT: Slater, Steven C.
APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Marry S.
APPLICANT: Gladman, Marry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR RILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11122
LENGTH: 306
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Best Local Similarity 38.5%;
Matches 115; Conservative 69
                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bacillus halodurans
US-10-369-493-17122
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Matches 119; Conserva
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Sequence 16570, Application US/10369493

Sequence 16570, Application US/10369493

Publication No. US2000233675A1

GENERAL INFORMATION:
APPLICANT: Clack of Seven C.
APPLICANT: Check of Seven C.
APPLICANT: Alanfan, Barry S.
APPLICANT: Check of Seven C.
APPLICANT: APPLICANT ON PLANTS WITH IMPROVED PROPERTIES
FILLE REFERENCE: 38-10(52052) B.
FILLE REPRENCE: 28-10(52052) B.
CURRENT APPLICANTON NUMBER: US/10/369,493

CURRENT FILING DATE: 2000-02-28
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                                                                                                                                                                                                                                                                                                    108 VTKKKIDEIVELVGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 YYIQADDIQALTR-----EAAAFRKVKVDEAEGGIEL--SIQKDEVPDLIKHLTDSGVRL 280
                                                                                                                                                                                                                                        62 TLLEPSSGEARVLGLDVVKDAREIRKRINLVAEGERTLYWRLTAYENLRYFASIYYIPRR 121
                                                                                                                                                                                                                                                                                                                             168 IREIRDYLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKR 227
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                                                                                                                            4 LLELKNVSKTIRGKKI------IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIV 51
                                                                                                                                                   ::|::|: | : ||| |||||||||:::
3 VIEVRNLRK-LYPKKIPLPPRKVEWFBALKGITFRVKKGELFGLLGPNGAGKTTTIKILT 61
                                                                                                                                                                                                                                                                                                                                                                                                                       1 LETLLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGE
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                                                                                31;
                                       Length 318;
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Best Local Similarity 46.2%; Pred. No. 5.2e-33;
Matches 98; Conservative 51; Mismatches 61; Indels
                                       . Score 491.5; DB 4; Length 3; Pred. No. 2.4e-33; 78; Mismatches 97; Indels
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16570
LENGTH: 221
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295 LSVEVKEPTLEDVFIKLT 312
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                                         31.9%;
                                       Query Match
Best Local Similarity 35.2
Matches 112; Conservative
JS-10-369-493-1336
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Sequence 136, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Check, Youngwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1336
                                                           APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Stater. Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1297
LENGTH: 308
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 KGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTRE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
32.0%; Score 493; DB 4; Length 308;
Best Local Similarity 36.4%; Pred. No. 1.7e-33;
Matches 118; Conservative 67; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 AAAFRKVKVDEAEGGIELSIQKDEVPDLIK---
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Sequence 1297, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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ORGANISM: Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Pyrococcus horikoshii
US-10-369-493-1297
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                                                                                        Sequence 21602 Application US/10369493

Fublication No. US2003023675A1

GENERAL INFORMATION:
APPLICANT: Gao, Yongwei

APPLICANT: Gaodman, Barry S.
APPLICANT: Goldman, Marry S.
TITLE OF INVENTION: Expression of MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: Gaodman, Soloso, 39

FILE REFERENCE: 36-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER: OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 EKGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKRYYIQADDTQALTR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 KQGKTVFFSSHILSEVEELADKVGIIVKGKLRTVGTL----EEIKKQYMELEGYEIKVE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 EAAAFRKVKVDE-----AEGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDR 293
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30.7%; Score 473; DB 4; Length 305;
Best Local Similarity 35.3%; Pred. No. 8.5e-32;
Matches 107; Conservative 77; Mismatches 103; Indels 16;
180 QERNITILISSHILAEIEQLVDRIGIIHEGKL 211
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Fublication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: HISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MSASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT PELLING DATE: 2002-05-29
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US-10-369-493-21602
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US-10-369-493-21602
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                                                                                                                                                                                                                                                                  Length 346;
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02 .
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12401
LENGTH: 346
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Job time : 187 secs
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Sequence 1154, Ap
Sequence 4274, Ap
Sequence 4310, App
Sequence 4310, Ap
Sequence 4310, Ap
Sequence 4592, A
Sequence 54801, Ap
Sequence 54801, Ap
Sequence 2603, Ap
Sequence 2603, Ap
Sequence 2603, Ap
Sequence 2868, Ap
Sequence 678, App
Sequence 678, App
Sequence 678, App
Sequence 628, Ap
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                                                                                                                        July 13, 2006, 13:50:52 ; Search time 29 Seconds (without alignments) 605.617 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-110-293-697-4208
US-110-471-571A-2868
US-10-471-571A-4896
US-10-471-571A-4896
US-10-471-571A-4896
US-10-471-571A-4896
US-10-471-571A-4996
US-10-471-571A-4996
US-10-471-571A-4996
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US-10-471-571A-4996
US-10-471-571A-4996
US-10-471-571A-4996
US-10-471-571A-4996
US-10-471-571A-496
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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45974, Ap 45974, Ap 195974, Ap 195976, Ap 195976, Ap 195976, Ap 195976, Ap 195976, Ap 19529, Ap 19559, Ap 
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US-10-471-571A-5186
US-11-056-358-45974
US-10-471-571A-1350
US-10-449-902-35418
US-10-449-902-4054
US-10-471-571A-2420
US-10-471-571A-2420
US-10-471-571A-252
US-10-471-571A-252
US-10-471-571A-252
US-10-471-571A-2720
US-10-471-571A-2720
US-10-953-349-6892
US-11-056-355B-73529
US-11-056-355B-73529
US-11-056-355B-85264
US-11-056-355B-85263
US-11-056-355B-85263
US-11-056-355B-85263
US-11-056-355B-85263
US-11-056-355B-85263
US-11-056-355B-85263
US-11-056-355B-85263
US-11-056-355B-85263
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## ALIGNMENTS

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64 CGVSVKENPEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVELVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 I-----NSKDSKSNIGALIENPGIYPFMSGYENLK---LLNESKNTQDIDKIVSQLHMD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3584, Application US/10471571A
| Publication No. US20060115490A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: CHIRON SpA
| TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
| FILE REPERENCE: PO26927W0
| CURRENT APPLICATION NUMBER: US/10/471,571A
| PRIOR PILING DATE: 2003-09-12
| PRIOR FILING DATE: 2001-03-27
| NUMBER OF SEQ ID NOS: 5642
| SEQ ID NO 3584
| LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VLIIEHLIKKIGNKTILEDVSFKLKRGQIVGLVGANGAGKTTLMKVILGYSSFQSGNFNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.7%; Score 411.5; DB 6; Length 231; Best Local Similarity 37.3%; Pred. No. 1.5e-21; Matches 84; Conservative 61; Mismatches 65; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 MAVIVSSHLLSEMELMCDRIAIIQNGKLRDIQHVHGPARDEKKRY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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LOCATION: (1)...(231)

OTHER INFORMATION: hypothetical protein

MS-10-471-571A-3584
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63 62

US-10-471-571A-1354 ; Sequence 1354, Application US/10471571A

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US-11-289-102-341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYAR-MIKGVIKKKIDEIVELVGLK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 NRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKG 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 716, Application US/10471571A
PUBLIcation No. US20060115490A1
GENERAL INFORMATION:
TITLE OF INVENTION: STAHYLOCCCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: STAHYLOCCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: STAHYLOCCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SEQ ID NO 716
SEQ ID NO 716
Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SIA
TITLE OF INVENTION: STARPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26927M0
CURRENT PILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqMin99, version 1.03
SEQ ID NO 1354
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                           Length 290;
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                                                                                                                                                                                                                                                                                                                                                                                         26.2%; Score 404.5; DB 6;
31.2%; Pred. No. 6e-21;
tive 76; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , LOCATION: (1). (232)
, OTHER INFORMATION: hypothetical protein US-10-471-571A-716
                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
LOCATION: (1).7(290)
OTHER INFORMATION: hypothetical protein
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US-10-471-571A-716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 GLARLGLSWYADRPAGTYSGGNKRKLATALALVGDPAVVFLDEPTTGMDPSARRFLWNSL 380
                                                                                                                                                                                                                                                                                      204 VLVLRNLTKVYRGQRMPAVDRLCLGIPPGECFGLLGVNGAGKTSTFRMVTGDTLASRGEA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || : :: || || | :| || || || 440 AARSQPAAAFV-------AAEFPGAELREAHGG-RLRFQ---LPPGGRCALARVFG 484
                                                                                                                                                                                        65 GVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMIKGVTKKKIDEIVELVGLKN 124
                                                                                                                                                                                                                              S LELKOVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
                                                                                                                            6 LVTENISKRFKNODVLKHINITLENNEVYGLLGINGAGKTTLMKIICGILQQDSGEIKLD 65
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  Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.7%; Score 349.5; DB 7; Length 5
30.2%; Pred. No. 9e-17;
cive 68; Mismatches 108; Indels
                                                Indels
25.5%; Score 392.5; DB 6; 38.0%; Pred. No. 3e-20; vative 55; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLIKHLIDSGVRLYEVKAVNKSLEDRFLEITADK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4274, Application US/11293697
; Publication No. US2006010537641
; Publication No. US2006010537641
; GRNERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT FAPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SEQ ID NOS: 5458
; SEQ ID NOS: 5458
; SEQ ID NOS: 5458
                                                                                                                                                                                                                                                                                                                                                                                                                       181 SIIISSHILSEIQVLADHIGIIHEGELK 208
                                                                                                                                                                                                                                                                                                                                                                                              185 AVIVSSHLLSEMELMCDRIALIONGKLR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.7
Best Local Similarity 30.2
Matches 101; Conservative
                                                     79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-11-293-697-4274
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-11-293-697-4274
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11;

22;

Length 299

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65 GVSVKENFEKAARHIGAIVENPELYKFLIGYQNLQQYARMTKGVIKCKIDEIV----ELV 120
                                                                                                                                                                                                                                                                                                                  121 GLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTR 180
                                                                                                                                                                                                                                                                                                                                                                                                             181 EKGMAVIVSSHLLSEMELMCDRIAIIQNGKL---RDIQHVHGPARDEKKRYYIQADDT-Q 236
                                                                                                                                                                                                                                                                                                                                                                                                                                         178 DWGSTIVYSSHRMEHVEELCDDVCILDKGQLVVSGDINHVR--ASNGNKKVVIESETTLP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 DLTNIRGI---IHSENMKQGLQLTIENEDVAKDIYQVVAHQGYVKRFQV--VEPSLQDIF 290
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                                                                                                                                                    3 LVIEHVTKRFGKMTAVNDISLKLESGKMLGFLGRNGAGKTTTFRMILGLSEPTEGHITYN 62
                                                                                                                         5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVC 64
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APPLICANT: National institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE REFERENCE: MOA-A020SY1-US
FILE REFERENCE: MOA-A020SY1-US
CURRENT APPLICATION NUMBER: UP 2002-203269
PRIOR PELICATION NUMBER: UP 2002-203269
PRIOR PELICATION NUMBER: UP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR PELING DATE: 2002-05-30
PRIOR PELING DATE: 2002-05-30
PRIOR PELING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                               63 G---KKLDKTMYNRIGYLPEERGLHGKLTVEEEL-KYLATLKGMSKTEIQQQISYMLERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 NVSKTIRGKK-----IIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTREAAAFRKVKVDBAEGGIELSIQKDEV-POLIKHLTDSG-VRLYEVKAVNKSLEDRF
                        21.9%; Score 338; DB 6; Length 29
30.5%; Pred. No. 2.5e-16;
tive 70; Mismatches 122; Indels
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29.4%; Pred. No. 3.2e-15;
tive 75; Mismatches 120;
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Best Local Similarity 29.44
Matches 96; Conservative
                                                                          94; Conservative
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291 IEKVGGKD 298
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US-10-449-902-43324
                                                   Best Local Similarity
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LENGTH: 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGEIAVCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 YLRKLTREKGMAVIVSSHLLSEMELMCDRIAIIQNGKLRDI---QHVHGP-ARDEKKRYY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 IQADDTQALTREAAAF-----RKVKVDEAEG-----GIELSIQKDEVPDLIKHLTDS 276
                                                                APPLICANT: Lee, Hyerim
APPLICANT: Lee, Hyerim
APPLICANT: Shaw, Peter M.
APPLICANT: Shaw, Peter M.
APPLICANT: Clark, Edwaw, Peter M.
APPLICANT: Clark, Edwaw,
TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
FILE REPERBRUCE: 10338 NP
CURRENT APPLICATION NUMBER: US/11/289,102
CURRENT FILING DATE: 2005-11-29
PRIOR PLILING DATE: 2005-11-39
PRIOR PLILING DATE: 2005-11-30
NUMBER OF SEQ ID NOS: 395
SOFTWARE: Patentin version 3.3
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Fublication No. US20060115490A1
Fublication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION:
FILE REFERENCE: POZ6927VO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT PLING DATE: 2003-09-12
FRIOR APPLICATION NUMBER: GB-0107661.1
FRIOR APPLICATION NUMBER: GB-0107661.1
FRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE SeqWin99, version 1.03
SEQ ID NO 4370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.5%; Score 346.5; DB 7;
32.8%; Pred. No. 6.2e-16;
ive 58; Mismatches 126;
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CCATION: (1)..(299)
CTHER INFORMATION: hypothetical protein
US-10-471-571A-4370
Sequence 341, Application US/11289102
Publication No. US20060121511A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1673 YGVDDYSVSQI--SLEQVFL 1690
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LENGTH: 1704
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35;

Indels

Length 949;

41;

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Length 304;

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120 VGLKNRINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDBPTNGLDPAGIREIRDYLRKLT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 CGVSVKENFEKA--ARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKID--EIVEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 54801, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

TILLE OF INVENTION: Foundation for Advancement of International Science.

TILLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFRENCE: MOA-A020591-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT PILING DATE: 2003-05-29

PRIOR PILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SEGUATION PARE PARENTED NOS: 56791

SEGUATED PARENTED PARENTED NOS: 56791
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76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 20.5%; Score 316.5; DB 7; Similarity 27.9%; Pred. No. 7.8e-15; 89; Conservative 64; Mismatches 125;
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FILE REFERENCE: 1055/256
CURRENT APPLICATION NUMBER: US/11/274,683
CURRENT FILING DATE: 2005-11-14
PRIOR APPLICATION NUMBER: US 60/627,752
PRIOR FILING DATE: 2004-11-12
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.3
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces sp. NRRL 30748
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Matches 89; Conserv
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Best Local Similarity
Matches 73; Conserv
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US-10-449-902-54801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 KLTREKGMAVIVSSHLLSEMELMCDRIALIQNGKLRDIQHVHGPARDEKKR---YYLQA- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |:: |::::| | |::|||: | |::|||: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           864 TISPEFEGEVENLARKLSPNARKVYHLSGTOKYELPKOOVRIADVFM-AVENFKRRTEVO 922
                                                                                                                          864 TTSPEFEGEVENLARKLSPNARKVYHLSGTOKYELPKOOVRIADVFM-AVENFKRRTEVO 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 VCGVSVKENFEKAARHIGAIVENPELYKFLTGYQNLQQYARMTKGVTKKKIDEIV-ELVG 121
          810 QAKRDR--AIVLTTHSMEEAEVLCDRLCIMVDGSLQCI----GTPKELIARYGGYYVLTM 863
                                                                       -----DDTQALTREAAA-FRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 44523, Application US/10449902

| Publication No. US20060123505A1
| Publication No. US20060123505A1
| GENERAL INFORMATION:
| APPLICANT: National Institute of Agrobiological Sciences.
| APPLICANT: Bio-oriented Technology Research Advancement Institution.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: The Institute of Physical and Chemical Research.
| APPLICANT: Foundation for Advancement of International Science.
| TILE REFERENCE: MOA-A0205Y1-US
| TILE REFERENCE: MOA-A0205Y1-US
| CURRENT FILING DATE: 2003-05-29
| PRIOR FILING DATE: 2003-05-29
| PRIOR PLING DATE: 2002-05-30
| PRIOR PLING DATE: 2002-05-30
| PRIOR PLING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
| SOFTWARE: PatentIn Ver. 2.1
| LENGTH: 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 NVSKTIRGKK-----IIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
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APPLICANT: Haltli, Bradley A
TITLE OF INVENTION: Elatophylin biosynthetic gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.5%; Score 331.5; DB 6;
29.4%; Pred. No. 3.2e-15;
tive 75; Mismatches 120;
                                                                                                                                                                                                                                                       285 A---VNKSLEDRFLEITADKEEAQHV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 923 AWGLADTTMEDVFVKVAKGAQSSEEL 948
                                                                                                                                                                                                                   285 A---VNKSLEDRFLEITADKEEAQHV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/11274683 Publication No. US20060141583A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Oryza sativa
US-10-449-902-44592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 96; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-11-274-683-30
                                                                               233
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138 RQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVIVSSHLLSEME 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 KVDEAEGGIELSIQKDEVP-DLIKHLTDSGVRLYEVK---AVNK-----SLEDRFLEIT 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CGVSVKENFEKAAR-HIGAIVENPELYKFLTGYQNLQQYARMTKGVTK----KKIDEIVEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3086, Application US/10471571A

Publication No. US20060115490A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: P026927WO

CURRENT FILING DATE: 2003-09-12

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 5642

SOFTWARE: SeqWin99, version 1.03

SEQ ID NO 3086

LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 KRKLCFALSMLGNPQITLLDEPSTGMDPKAKQHMWRAIRTAFKNRKRAAILTTHYMEEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VIKFKNVTKRYGKHVAVDNISFNINEGEFFVLIGPSGCGKTTTLKMINRLIHLSEGYIYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LSPDVRAGBIFGFLGPNGAGKTTTIRMIVGHMSITAGBIAVCGVSVK-ENFEKAARHIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 IVENPELYKPLTGYQNLQQYARMTKGVT----KKKIDEIVELVGLKONRINDKVKTYSLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 559;
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                                                                                                                                                                                                                                                                                                                                                                                            19.7%; Score 303.5; DB 7; Length 28.9%; Pred. No. 1.4e-13; tive 73; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.2%; Pred. No. 9.2e-14;
Matches 89; Conservative 72; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1). (325)
OTHER INFORMATION: hypothetical protein
   CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus
                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2603
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 88; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADKEE 303
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                                                                                                                                                                                                                      LENGTH: 559
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                                                                                                                                                                                                                                                       78 HIGAIVENPELYKFLIGYQNLQQYARMTKGVTKKKIDEIVE----LVGLKNRINDKVKTY 133
                                                                                                                                                                                                               134 SLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVIVSSHLL 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 KAARHIGAIVENPELYKFLTGYONLOOYARMTKGVTKK----KIDEIVELVGLKNRINDK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKTYSLGMRQRLGLAQSLLHDPKLLILDEPINGLDPAGIREIRDYLRKLTREKGMAVIVS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 SHLLSEMELMCDRIAIIQNGKLR---DIQHVHGPARDEKKRYYI---QADDTQALTRBAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AFRKVKVDEA--EGGIELSIQKDEVPDL-----IKHLTDSGVRLYEVKAVNKS 289
                                                                                                                                        609 MIGVCPQFDILWDALTAKEHMELFASI-KGLPPSTIKSVAEOSLIOVKLSOAANVRAGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGKKI-IEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVKENFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4228, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A01106
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-12-05
PRIOR FILING DATE: 2005-12-05
SOFTWARE: PATENTIN NUMBER: US/10/108,260
FROM FILING DATE: 2005-12-05
SOFTWARE: PATENTIN VONES: 2458
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Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE SHERENCE: H1-A01106
CURRENT APPLICATION NUMBER: US/11/293,697
                                                                                                                                                                                                                                                                                                                                                           SEMELMCDRIAIIQNGKLRDI 214
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780 LEKVFLELSKEQE 792
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Best Local Similarity 30.78
Matches 96; Conservative
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LENGTH: 815
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SDXPISDYPVYEMRWDIGYVLQQIALFPHMTIKENIAQVPQMKKWKEKDIDKRVDELLEM 120
                                                                      231
                                                                                                                                          EIAVCGVSV----KENFEKAARHIGAIVENPELYKFLTGYQNLQ----OYARMTKGVTKKK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ALELVELVGLKGREKAYPSELSGGOKORVGIARALANDPTVLLCDEATSALDPOTTDEIL 180
                                                    VGL-----KORINDKVKTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDY 174
                                                                                                                                                                                            --ADDTQALTREAAAFRKV----KVDEAEGGIELSIQKDEVP-DLIKHLTDSGVRLYEVK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LLELKNVSKTIRGKK----IIEGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRKLTREKGMAVIVSSHLLSEMELMCDRIAIIONGKLRDIQHVHGPARDEKKRYYIQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P02692740
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT PILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR PELICATION NUMBER: GB-0107661.1
PRIOR PERO PS SEQ ID NOS: 5642
SOFTWARE: SegWin99, version 1.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE

LOCATION: (1)...(341)

COTHER INFORMATION: ABC transporter ATP-binding
US-10-471-571A-2868
                                                                                                                                                                                                                                                             --AVNKSLEDR---FLEITADKEEAQH 306
                                                                                                                                                                                                                                                                                  EDSVGQYVIDRKDIFKYLSQKKEVAQH 324
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2868, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus aureus
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US-10-471-571A-2868
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US-10-471-571A-678
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APPLICANT: CHIRON SPA TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS FILE REFERENCE: P026927WO

Sequence 678, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:

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75 AARHIGAIVENPELYKFLTGYQNLQQYARMT-----KGVTKKKIDEIVELVGLKNRIN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 DKVKTYSLGMRORLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREKGMAVI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GKK-IIBGLSFDVRAGEIFGFLGPNGAGKTTTIRMIVGHMSITAGEIAVCGVSVKENFEK 74
                                                                                                                                                                                                                                                                                                                                                                                                          23 GKRPVIKDINFELMKGEIVGLIGLMGAGKSTTIKHMLGLLTPMEGSLSISDININDDIEA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 VSSHLLSEMELMCDRIAIIQNGK-----LRDIQHVHGPARDEKKRYYIQADDTQA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.5%; Pred. No. 2.2e-13;
Matches 68; Conservative 62; Mismatches 87; Indels
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 678
                                                                                                                                                                                                                                ; LOCATION: (1). (256)
; OTHER INFORMATION: ABC transporter ecsA
US-10-471-571A-678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: July 13, 2006, 13:54:27
le : 30 secs
                                                                                                                                                                              ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
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